



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143132

TO: Janet Epps-Ford
Location: rem/2c05/2c18
Art Unit: 1635
Wednesday, July 13, 2005

Case Serial Number: 09/753169

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Epps-Ford,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524



THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169A-1
Perfect score: 20
Sequence: 1 ctaacacagtcattgtcca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	Az46971 Bcl-Xl MR
2	20	100.0	559	12	Ach73889 Human gen
c 3	20	100.0	737	2	Aa81699 Human thy
c 4	20	100.0	737	10	Abz83507 Toxicolog
c 5	20	100.0	737	11	Adi32132 Human cdn
c 6	20	100.0	863	12	Adh52632 Chinese h
c 7	20	100.0	926	2	Aa81698 Human thy
c 8	20	100.0	926	2	Aat40079 Bcl-XL ge
c 9	20	100.0	926	3	Aaz93614 Bcl-x gen
c 10	20	100.0	926	4	Aas15189 Human bcl
c 11	20	100.0	926	4	Aac90810 Human bcl
c 12	20	100.0	926	6	Abk84766 Human cdn
c 13	20	100.0	926	8	Abt16641 Human bcl
c 14	20	100.0	926	10	Adb56779 Human bcl
c 15	20	100.0	926	10	Aad64187 Human bcl
c 16	20	100.0	926	11	Adi32104 Human cdn
c 17	20	100.0	926	12	Adh52630 Human ant
c 18	20	100.0	926	12	Adoi9990 Human pro
c 19	20	100.0	926	12	Adp13351 Renal cel
c 20	20	100.0	1384	2	Aav17638 Mouse BCL
c 21	20	100.0	1466	10	Ade85177 Farnesyl

c 22	20	100.0	1742	4	Aaf75960 Rat wild-
c 23	20	100.0	1748	10	Adb58615 Toxigenic
c 24	20	100.0	1748	10	Adb53263 Primary r
c 25	20	100.0	2386	10	Adg89403 Cancer de
c 26	20	100.0	2386	12	Adn04260 Antipsori
c 27	20	100.0	2575	12	Adoi9866 Human PRO
c 28	18	90.0	21	6	Adv73037 Nucleotid
c 29	16.8	84.0	591	9	Adb10715 Alloiococ
c 30	16.8	84.0	591	9	Adb10717 Alloiococ
c 31	16.8	84.0	1509	6	Abk99834 Babesia c
c 32	16.8	84.0	1950	6	Abk99832 Babesia c
c 33	16.8	84.0	1959	6	Abk99865 Babesia c
c 34	16.8	84.0	2000	12	Adj41501 Plant cdn
c 35	16.8	84.0	2122	6	Abk99833 Babesia c
c 36	16.8	84.0	2157	6	Abk99831 Babesia c
c 37	16.8	84.0	2190	6	Abk99835 Babesia c
c 38	16.8	84.0	6509	6	Abk99835 Human imm
c 39	16.8	84.0	110000	9	Abk99835 Human imm
c 40	16.4	82.0	638	6	Abz15553 Arabidops
c 41	16.4	82.0	996	4	Aah71294 Human cer
c 42	16.4	82.0	2403	12	Adj40060 Plant cdn
c 43	16	80.0	20	3	Aaz93625 Antisense
c 44	16	80.0	20	5	Aah27670 Human bcl
c 45	16	80.0	20	10	Aad64198 Human bcl

ALIGNMENTS

RESULT 1
AAZ46971
ID AAZ46971 standard; DNA; 20 BP.
XX AC AAZ46971;
XX DT 14-APR-2000 (first entry)
XX DE Bcl-Xl mRNA specific antisense oligo A.
XX KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;
XX KW lung; bladder; bcl-2; vascular lesion; antisense; ss.
XX OS Homo sapiens.
XX PN WC200001393-A2.
XX PD 13-JAN-2000.
XX PF 02-JUL-1999; 99WO-US015250.
XX PR 02-JUL-1998; 98US-00109614.
XX PA (UYCO) UNIV COLUMBIA NEW YORK.
XX PI Stein CA;
XX DR WPI; 2000-137140/12.
XX PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.
XX PS Claim 1; Fig 1; 69pp; English.
XX CC The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
 CC represent antisense oligos specific for the bcl-X1 mRNA
 XX
 SQ Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
 |||||
 Db 1 CTCACACGATCCATTGTCCA 20

RESULT 2

ACH73889
 ID ACH73889 standard; DNA; 559 BP.

XX
 AC ACH73889;

DT 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #7084.

XX Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

XX (RANK/) RANK D R.

XX (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

XX Claim 15; SEQ ID NO 7084; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 559;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
 |||||
 Db 178 CTCACACGATCCATTGTCCA 197

RESULT 3

AAQ81699/c

ID AAQ81699 standard; DNA; 737 BP.

XX AAQ81699;

DT 25-MAR-2003 (revised)

DT 10-AUG-1995 (first entry)

XX Human thymus BCL-XS DNA.

XX BCL-XS; apoptosis; cell death; cancer; neurodegenerative disease;
 KW autoimmune disease; Parkinson disease; amyotrophic lateral sclerosis;
 KW multiple sclerosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 135..647
 FT /*tag= a

XX WO9500642-A1.

XX 05-JAN-1995.

XX 22-JUN-1994; 94WO-US007089.

XX 22-JUN-1993; 93US-00081448.

XX (ARCH-) ARCH DEV CORP.

XX (UNMI) UNIV MICHIGAN.

XX Thompson CB, Boise LH, Nunez G;

XX WPI; 1995-052079/07.

XX P-PSDB; AAR68888.

XX New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis -
 PT and related vectors, recombinant cells and antibodies, useful in assay
 PT and for control of cell death in e.g. neuronal cells, lymphocytes and
 PT cancers.

XX Claim 5; Page 98; 127pp; English.

XX This DNA may be expressed recombinantly for the production of a BCL-X

CC protein, particularly with pcMV plasmids as vectors for expression in
CC mammalian cell cultures. The protein has particular application in cancer
CC cells (failure of programmed cell death (PCD)) or neurodegenerative and
CC autoimmune diseases (premature PCD), e.g. Parkinson's disease,
CC amyotrophic lateral sclerosis and multiple sclerosis. (Updated on 25-MAR
CC -2003 to correct PN field.)

XX Sequence 737 BP; 181 A; 209 C; 198 G; 149 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 737;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCAAGTCCATTGTCCA 20

Db 116 CTCAACCAAGTCCATTGTCCA 97

RESULT 4

ABZ83507/c

ID ABZ83507 standard; cDNA; 737 BP.

AC ABZ83507;

XX 14-MAY-2003 (first entry)

XX Toxicologically relevant human nucleotide sequence #666.

DE Toxicologically relevant gene; toxicological response; gene; ss.

XX Homo sapiens.

XX WO2003016500-A2.

XX 27-FEB-2003.

XX 16-AUG-2002; 2002WO-US026514.

XX 16-AUG-2001; 2001US-0313080P.

XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;
PI Alen P;

XX WPI; 2003-268322/26.

XX Determining a toxicological response to an agent, useful for screening of
PT drugs, comprises comparing the expression profile of one or more human
PT toxic response genes to a reference gene expression profile indicative of
PT toxicity.

PS Claim 1; Page 226; 455pp; English.

XX The present invention describes a method (M1) for determining a
CC toxicological response to an agent, which comprises comparing the
CC expression profile of one or more human toxic response genes to a
CC reference gene expression profile indicative of toxicity, and so
CC determining the presence of a toxic response to the agent. Also
CC described: (1) an array comprising one or more polynucleotides selected
CC from the genes corresponding to the partial sequences given in ABZ82842
CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC ; and (2) determining if a gene putatively identified to be a toxic
CC response gene plays a role on toxic response pathways by determining the
CC expression profile of the gene after exposure of cells or a human subject
CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC exposing cells to an agent or isolating cells from a human subject who
CC was exposed to an agent; (b) obtaining the test gene expression profile
CC for a putatively identified toxic response gene after exposure to a known
CC toxic pharmaceutical or industrial agent; and (c) comparing the test
CC profile to the expression profile of a gene with a similar function or
CC comparing the test profile to the expression profile of that gene after
CC exposure to other known toxic compounds. The methods are useful for

CC predicting and determining toxicological responses on a cellular, organ
CC or system level. The arrays comprising the human genes are useful for
CC toxicological screening of drugs, pharmaceutical compounds and chemicals
XX Sequence 737 BP; 181 A; 209 C; 198 G; 149 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 737;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCAAGTCCATTGTCCA 20

Db 116 CTCAACCAAGTCCATTGTCCA 97

RESULT 5

ADI32132/c

ID ADI32132 standard; cDNA; 737 BP.

XX ADI32132;

XX 17-JUN-2004 (first entry)

XX Human cDNA #1458.

XX Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cyrostatic.

XX Homo sapiens.

XX US6607879-B1.

XX 19-AUG-2003.

XX 09-FEB-1998; 98US-00023655.

XX 09-FEB-1998; 98US-00023655.

XX (INCY-) INCYTE CORP.

XX Cocks BG, Stuart SG, Seilhamer JJ;

XX WPI; 2003-895307/82.

XX A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.

PS Claim 1; SEQ ID NO 1458; 50pp; English.

XX The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in

CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 737 BP; 181 A; 209 C; 198 G; 149 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 11; Length 737;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGAGTCATTGTCCA 20
Db 116 CTCACACGAGTCATTGTCCA 97

RESULT 6

ADH52632/c

ID ADH52632 standard; DNA; 863 BP.

XX AC ADH52632;

XX DT 25-MAR-2004 (first entry)

XX DE Chinese hamster anti-apoptosis bcl-xL wild-type DNA.

XX KW mammalian myeloma host cell; protein production; anti-apoptosis;
XX KW cell death; Chinese hamster; bcl-xL; wild-type; ds; gene.

XX OS Cricetulus griseus.

XX PN US2003219871-A1.

XX PD 27-NOV-2003.

XX PF 28-MAR-2003; 2003US-00402017.

XX PR 02-APR-2002; 2002US-0369307P.

XX PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.

XX PI Enkel B, Meents H, Fussenegger M;

XX DR WPI: 2004-033642/03.

XX DR P-PSDB; ADH52633.

XX PT New genetically engineered hamster or murine myeloma host cells
XX PT comprising enhanced levels of active anti-apoptosis genes, useful for
XX PT producing complex protein therapeutics.

XX PS Claim 57; SEQ ID NO 3; 46pp; English.

XX CC The invention relates to a novel mammalian host cell for producing
XX CC protein therapeutics. The host cell comprises a hamster or a murine
XX CC myeloma cell that is genetically modified by introduction of nucleic acid
XX CC sequences encoding an anti-apoptosis gene, a selectable amplifiable
XX CC marker gene and at least one gene of interest. The host cell of the
XX CC invention may be useful for producing at least one protein encoded by a
XX CC gene of interest. The DNA, polypeptide and the methods may be used for
XX CC inhibiting or delaying cell death. The current sequence is that of the
XX CC Chinese hamster anti-apoptosis bcl-xL wild-type DNA of the invention.

XX SQ Sequence 863 BP; 212 A; 227 C; 247 G; 177 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 863;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGAGTCATTGTCCA 20

Db 51 CTCACACGAGTCATTGTCCA 32

RESULT 7

AAQ81698/c

ID AAQ81698 standard; DNA; 926 BP.

XX AC AAQ81698;

XX DT 25-MAR-2003 (revised)

XX DT 10-AUG-1995 (first entry)

XX DE Human thymus BCL-XL DNA.

XX KW BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease;

XX KW autoimmune disease; Parkinson disease; amyotrophic lateral sclerosis;

XX KW multiple sclerosis; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 135..836

XX FT /*tag= a

XX PN WO9500642-A1.

XX PD 05-JAN-1995.

XX PF 22-JUN-1994; 94WO-US007089.

XX PR 22-JUN-1993; 93US-00081448.

XX PA (ARCH-) ARCH DEV CORP.

XX PA (UNMI) UNIV MICHIGAN.

XX PI Thompson CB, Boise LH, Nunez G;

XX DR WPI; 1995-052079/07.

XX DR P-PSDB; AAR68887.

XX PT New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis -
XX PT and related vectors, recombinant cells and antibodies, useful in assay
XX PT and for control of cell death in e.g. neuronal cells, lymphocytes and
XX PT cancers.

XX PS Claim 5; Page 94; 127pp; English.

XX CC This DNA may be expressed recombinantly for the production of a BCL-X
XX CC protein, particularly with pcmv plasmids as vectors for expression in
XX CC mammalian cell cultures. The protein has particular application in cancer
XX CC cells (failure of programmed cell death (PCD)) or neurodegenerative and
XX CC autoimmune diseases (premature PCD), e.g. Parkinson's disease,
XX CC amyotrophic lateral sclerosis and multiple sclerosis. (Updated on 25-MAR
XX CC -2003 to correct PN field.)

XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 926;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGAGTCATTGTCCA 20

Db 116 CTCACACGAGTCATTGTCCA 97

RESULT 8

AAT40079/c

ID AAT40079 standard; cDNA; 926 BP.

XX AC AAT40079;

XX XX

```

DT 30-MAR-1997 (first entry)
XX DE Bcl-XL gene.
XX KW Human; bcl-XL; T-lymphocyte; cell death; gene therapy; HIV; AIDS;
XX KW antisense; immune disorder; autoimmune disease; graft rejection;
XX KW graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 135..836
XX FT /*tag= a
XX FT /product= "Human bcl-XL protein"
XX PN WO9634956-A1.
XX XX
XX PD 07-NOV-1996.
XX PF 02-MAY-1996; 96WO-US006203.
XX PR 04-MAY-1995; 95US-00435518.
XX PR 07-JUN-1995; 95US-00481739.
XX PA (USNA ) US SEC OF NAVY.
XX PA (ARCH-) ARCH DEV CORP.
XX PI June CH, Thompson CB;
XX DR WPI; 1996-506159/50.
XX DR P-PSDB; AAW05821.
XX PT Inducing or preventing death of T cells by bcl-XL protein regulation -
XX PT used to increase survival of HIV infected cells or to down-regulate
XX PT immune responses in immune diseases.
XX PS Disclosure; Page 51-52; 76pp; English.
XX CC This sequence encodes human bcl-XL protein, which protects T-lymphocytes
XX CC against cell death. The genomic bcl-X gene may produce 2 different mRNAs,
XX CC one encoding a long form (bcl-XL), the other a short form (bcl-XS),
XX CC lacking a stretch of 63 amino acids, by differential splicing of the 2nd
XX CC coding exon to a more proximal 5'-splice donor within the 1st coding
XX CC exon. Bcl-XS acts as a dominant negative regulator to bcl-XL activity, so
XX CC it is preferable to use the bcl-XL cDNA for expression. The gene may be
XX CC modified to facilitate interaction with costimulatory Bax protein and
XX CC inhibit interaction with antagonistic Bad protein, by modification of the
XX CC Bcl-2 homology domains BH1 and/or BH2. The bcl-XL gene may be introduced
XX CC into T-cells in vivo or ex vivo via gene transfer using a vector for HIV
XX CC infection gene therapy, to augment intracellular bcl-XL protein levels
XX CC and protect from cell death. A corresponding antisense oligonucleotide or
XX CC expression vector may be used in gene therapy of e.g. autoimmune disease,
XX CC graft rejection or graft-versus-host disease, to induce cell death (e.g.
XX CC apoptosis) and down-regulate the immune response in a T-lymphocyte
XX CC population
XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 926;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCAAGTCCTGTCCTCA 20
DB 116 CTCAACCAAGTCCTGTCCTCA 97

RESULT 9
AAZ93614/c
ID AAZ93614 standard; DNA; 926 BP.
XX AC AAZ93614;
XX DT 16-JAN-2002 (first entry)
XX XX

DT 16-AUG-2000 (first entry)
XX DE Bcl-x gene.
XX KW Bcl-x; bcl-xs; antisense; therapy; apoptosis; splice site;
XX KW cell signalling molecule; ultraviolet radiation; UV; cancer;
XX KW chemotherapy; cytokine; human; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 135..836
XX FT /*tag= a
XX FT /product= "Bcl-x polypeptide."
XX PN WO200020432-A1.
XX XX
XX PD 13-APR-2000.
XX PF 28-SEP-1999; 99WO-US022448.
XX PR 07-OCT-1998; 98US-00167921.
XX PR 26-MAR-1999; 99US-00277020.
XX PR 02-JUN-1999; 99US-00323743.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang Q;
XX DR WPI; 2000-303730/26.
XX DR P-PSDB; AAY83223.
XX PT Antisense oligonucleotides targeted to, and capable of inhibiting the
XX PT expression of, bcl-x nucleic acids, useful for sensitizing cancer cells
XX PT to apoptotic agents.
XX PS Disclosure; Page 102-103; 115pp; English.
XX CC Antisense inhibition of bcl-x and bcl-xs expression results in apoptosis.
XX CC Antisense oligonucleotides directed against bcl-x alter the ratio of bcl-
XX CC x isoforms expressed by a cell or tissue (i.e. increases or decreases the
XX CC ratio of bcl-xl to bcl-xs expressed) by altering the splicing of the RNA
XX CC encoding bcl-x. The antisense oligonucleotide is specifically targeted to
XX CC a transcript comprising two splice sites which when contacted with the
XX CC transcript, reduces the relative frequency of splicing at the second
XX CC splice site so that the resulting ratio of RNA splice products is
XX CC altered. The use of antisense compounds sensitises cells to the effects
XX CC of apoptotic stimulants such as a cellular signaling molecule,
XX CC ultraviolet radiation, a cancer chemotherapeutic drug (e.g. VP-16,
XX CC cisplatin or taxol), ceramide (e.g. staurosporine) or a cytokine which
XX CC causes mitochondrial dysfunction (especially loss of mitochondrial
XX CC membrane function). The antisense oligonucleotides may have a therapeutic
XX CC role in the treatment of cancer
XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 926;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCAAGTCCTGTCCTCA 20
DB 116 CTCAACCAAGTCCTGTCCTCA 97

RESULT 10
AAS15189/c
ID AAS15189 standard; cDNA; 926 BP.
XX AC AAS15189;
XX DT 16-JAN-2002 (first entry)
XX XX

```

DE Human bcl-x cDNA.
XX Human; antisense; IL-5R; bcl-x; ss; antiinfection; antiinflammatory;
KW cytostatic; inflammation; infection; tumour.
XX Homo sapiens.
PN WO200172765-A1.
XX 04-OCT-2001.
XX 28-MAR-2000; 2000WO-US008174.
XX 28-MAR-2000; 2000WO-US008174.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Crooke ST, Manoharan M, Wyatt JR, Baker BF, Monia BP;
PI Freier SM, McKay R, Karras JG;
XX WPI; 2001-626250/72.
XX Controlling cell behavior, useful e.g. for treatment of tumors, by
PT modulating processing, e.g. splicing, of specific mRNA sequences with non
PT -cleaving antisense agents.
XX Example 15; Page 113; 121pp; English.
XX The invention relates to controlling cell behaviour by modulating the
CC processing of a selected wild-type mRNA target in the cell, is new. The
CC mRNA is bound to a specific-binding antisense compound that does not
CC cleave bound mRNA. The antisense oligonucleotides are useful as research
CC reagents, diagnostic agents (in hybridisation assays), and for treatment
CC or prevention of diseases, e.g. to prevent or delay infections,
CC inflammation and tumours. The present sequence is the cDNA for the human
CC bcl-x which is a target for antisense oligonucleotides if the invention
XX
SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 926;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCACACGATCCATTGTCCA 20
Db 116 CTCACACGATCCATTGTCCA 97
RESULT 11
AAC90810/c
ID AAC90810 standard; cDNA; 926 BP.
XX AAC90810;
AC
XX 16-MAR-2001 (first entry)
DT
XX Human Bcl-xL nucleotide sequence SEQ ID NO:3.
DE
XX Human; Bcl-2; Bcl-xL; Bax; VDAC; apoptosis inhibitor; detection;
KW apoptosis promoter; diagnosis; ss.
KW
XX Homo sapiens.
OS
XX JP2000287689-A.
PN
XX 17-OCT-2000.
PD
XX 08-APR-1999; 99JP-00101888.
PF
XX 08-APR-1999; 99JP-00101888.
PR
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA
XX

DR WPI; 2001-065575/08.
DR P-PSDB; AAB50538.
XX Screening of an apoptosis inhibitor or promoter which can be used as a
PT drug and a diagnostic agent for various diseases caused by apoptosis
PT inhibition or apoptosis promotion.
XX Claim 16; Page 14-15; 22pp; Japanese.
PS
XX The present invention describes a method for screening for an apoptosis
CC inhibitor or an apoptosis promoter in which VDAC-liposome, an index
CC substance which can pass VDAC and a sample are incubated and the change
CC in the concentration of the index substance during the incubation is
CC detected to judge the presence of apoptosis inhibition or apoptosis
CC promotion. The apoptosis inhibitor or the apoptosis promoter can be used
CC as a drug and a diagnostic agent for various diseases caused by apoptosis
CC inhibition or apoptosis promotion. The present sequence encodes the human
CC Bcl-xL protein, which is an apoptosis inhibitor used in the
CC exemplification of the present invention
XX
SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 926;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCACACGATCCATTGTCCA 20
Db 116 CTCACACGATCCATTGTCCA 97
RESULT 12
ABK84766/c
ID ABK84766 standard; cDNA; 926 BP.
XX
AC ABK84766;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #1337.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
XX WO200228999-A2.
PN
XX 11-APR-2002.
PD
XX 03-OCT-2001; 2001WO-US030821.
PF
XX 03-OCT-2000; 2000US-0237189P.
PR
XX (GENE-) GENE LOGIC INC.
PA
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
PI
XX WPI; 2002-435328/46.
DR
XX Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX
PS Claim 1; SEQ ID NO 1337; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation

CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 926;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCACACGATCCATTGTCCA 20
Db |||||
116 CTCACACGATCCATTGTCCA 97

RESULT 13

ABT16641/c
ID ABT16641 standard; DNA; 926 BP.

XX AC ABT16641;

XX DT 03-APR-2003 (first entry)

XX DE Human bcl-2 gene SEQ ID No 3.

XX KW Anti-tumour; DNazyme; bcl-2 gene; tumour; malignant; chemotherapy;
XX radiation therapy; catalytic domain; enzyme; human; ds.

XX OS Homo sapiens.

XX PN WO200299090-A1.

XX PD 12-DEC-2002.

XX PF 07-JUN-2002; 2002WO-AU000739.

XX PR 07-JUN-2001; 2001AU-00005527.

XX PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.

XX PI Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;

DR WPI; 2003-140617/13.

XX PT Novel DNazyme useful for treating tumors, and for enhancing the
XX sensitivity of malignant or virus infected cells to therapy, comprises a
XX catalytic domain and binding domain contiguous to the catalytic domain.

XX PS Disclosure; Page 44; 67pp; English.

XX CC The invention relates to a DNazyme which specifically cleaves mRNA
CC transcribed from a member of the bcl-2 gene family. The DNazymes comprise
CC a catalytic domain, binding domains contiguous with the 5' and 3' end of
CC the catalytic domain, and therefore hybridise with, the two regions
CC immediately flanking the purine residue of the cleavage site within the
CC bcl-2 gene family mRNA, at which DNazyme-catalysed cleavage is desired. A
CC pharmaceutical composition comprising a DNazyme of the invention is
CC useful for treating tumors in a subject, and for enhancing the
CC sensitivity of malignant or virus infected cells in diagnostics, therapeutics,
CC prophylaxis, research agents and in kits. The DNazymes are also useful
CC for increasing the susceptibility of tumour cells to anti-tumour
CC therapies such as chemotherapy and radiation therapy. This polynucleotide
CC sequence represents a human bcl-2 gene of the invention

XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 926;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCACACGATCCATTGTCCA 20
Db |||||
116 CTCACACGATCCATTGTCCA 97

RESULT 14

ADD56779/c

ID ADD56779 standard; DNA; 926 BP.

XX AC ADD56779;

XX DT 15-JAN-2004 (first entry)

XX DE Human bcl-xL nucleic acid sequence #SEQ ID 1.

XX KW Cytostatic; murine myeloma cell; anti-apoptosis gene;
XX biopharmaceutical protein; bcl-xL; apoptosis; ds.

XX OS Homo sapiens.

XX PN EP1348758-A1.

XX PD 01-OCT-2003.

XX PF 28-MAR-2002; 2002EP-00007144.

XX PR 28-MAR-2002; 2002EP-00007144.

XX PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.

XX PI Ehenkel B, Meents H, Fussenegger M;

XX DR WPI; 2003-781115/74.

XX PT New genetically modified host cells comprising nucleic acid sequences
XX that encode for an anti-apoptosis gene, a selectable amplifiable marker
XX gene or at least one gene, useful for producing biopharmaceutical
XX proteins.

XX PS Claim 9; SEQ ID NO 1; 42pp; English.

XX CC The invention relates to a hamster host cell or a murine myeloma cell
XX genetically modified by introducing nucleic acid sequences that encode
XX for an anti-apoptosis gene, a selectable amplifiable marker gene or at

CC least one gene of interest. The cells are useful for the production of at
 CC least one protein encoded by a gene of interest, particularly for the
 CC production of biopharmaceutical proteins. The genetically engineered host
 CC cells have improved survival properties and enhanced level of active anti
 CC -apoptosis genes compared to non-transfected as well as non-amplified
 CC parental cells. The current sequence represents a bcl-xL nucleic acid
 CC sequence.

XX
 SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 926;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCCAGTCCATTGTCCA 20
 |||||
 Db 116 CTCAACCCAGTCCATTGTCCA 97

RESULT 15

AAD64187/c
 ID AAD64187 standard; DNA; 926 BP.

XX AC AAD64187;

DT 12-FEB-2004 (first entry)

XX DE Human bcl-x DNA.

XX KW Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;
 KW retinitis pigmentosa; myocardial infarction; neuroprotective; cytosstatic;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW acquired immune deficiency syndrome; neurodegenerative disorder; AIDS;
 KW neurotropic; anticonvulsant; vasotropic; therapy; cerebroprotective;
 KW stroke; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT CDS 135..836

FT /*tag= a
 FT /product= "Human bcl-x protein"

XX PN US2003191300-A1.

XX PD 09-OCT-2003.

XX PF 21-NOV-2002; 2002US-00302262.

XX PR 07-OCT-1998; 98US-00167921.

PR 26-MAR-1999; 99US-00277020.

PR 02-JUN-1999; 99US-00323743.

XX PR 12-DEC-2000; 2000US-00734846.

PA (BENN/) BENNETT C F.

PA (DEAN/) DEAN N M.

PA (MONI/) MONIA B P.

PA (NICK/) NICKOLOFF B J.

XX PA (ZHAN/) ZHANG Q Q.

PI Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;

XX DR WPI; 2003-864192/80.

DR P-PSDB; ABW02410.

XX Compound useful for treating reduced apoptotic conditions e.g. cancer

PT comprises nucleobases targeted to nucleic acid molecule encoding human

PT gene encoding intracellular membrane protein.

XX Claim 1; SEQ ID NO 1; Opp; English.

XX The present invention relates to methods for modulating the expression of

CC bcl-x. The invention is useful for sensitising cancer cells such as

CC glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet
 CC radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention
 CC is useful for treating acquired immune deficiency syndrome (AIDS),
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy
 CC and ischaemia such as myocardial infarction and stroke. The present
 CC sequence is human bcl-x DNA

XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 926;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCCAGTCCATTGTCCA 20
 |||||
 Db 116 CTCAACCCAGTCCATTGTCCA 97

Search completed: February 4, 2005, 21:52:35

Job time : 263.033 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 480.738 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169a-1
Perfect score: 20
Sequence: 1 ctcaaccagtcattgtcca 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	BD235149
2	20	100.0	20	6	BD235162 Oligonucl
3	20	100.0	20	6	BD235163 Oligonucl
4	20	100.0	137	9	AY263337 Homo sapi
5	20	100.0	328	9	AY263336
6	20	100.0	388	9	AY263335 Homo sapi
7	20	100.0	512	6	CQ727769 Sequence
8	20	100.0	737	6	AR054022
9	20	100.0	737	6	AR172595
10	20	100.0	737	6	IS2012
11	20	100.0	737	6	AR371662
12	20	100.0	737	6	AR380913
13	20	100.0	737	9	HSBCLXS
14	20	100.0	764	10	RNU10579
15	20	100.0	765	4	AF164517
16	20	100.0	863	6	AX925688
17	20	100.0	926	6	AR054021
18	20	100.0	926	6	AR118504
19	20	100.0	926	6	AR124952

c 20	20	100.0	926	6	AR144311
c 21	20	100.0	926	6	AR172594
c 22	20	100.0	926	6	BD243042
c 23	20	100.0	926	6	CO765842
c 24	20	100.0	926	6	E58777
c 25	20	100.0	926	6	IS2011
c 26	20	100.0	926	6	AR371661
c 27	20	100.0	926	6	AR380885
c 28	20	100.0	926	6	AX839772
c 29	20	100.0	926	6	AX925686
c 30	20	100.0	926	9	HSBCLXL
c 31	20	100.0	979	10	MUSECLX
c 32	20	100.0	1011	9	HUMBCLXP
c 33	20	100.0	1235	10	MMU10102
c 34	20	100.0	1384	6	AR242207
c 35	20	100.0	1384	10	MMU51277
c 36	20	100.0	1466	6	AX775078
c 37	20	100.0	1466	10	MMU51278
c 38	20	100.0	1742	6	BD012974
c 39	20	100.0	1742	6	BD013799
c 40	20	100.0	1742	10	RNU72350
c 41	20	100.0	1748	6	AX827805
c 42	20	100.0	1748	10	RNU72349
c 43	20	103.0	1911	10	MMBCLAP1
c 44	20	100.0	2097	10	MMU51279
c 45	20	100.0	2375	10	AY141038

ALIGNMENTS

RESULT 1
BD235149
LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION BD235149
VERSION BD235149.1 GI:33044919
KEYWORDS JP 2002519048-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Stein, C.A.
TITLE Oligonucleotide inhibitors of bcl-xL
JOURNAL Patent: JP 2002519048-A 1 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT OS Artificial Sequence
PN JP 2002519048-A/1
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN

PC C12N15/09, A61K9/127, A61K31/711, A61K31/712, A61K31/7125, PC
A61K47/42,
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCAACCAGTCATTGTCCA 20
|||||

Db	1	CTCAACCGAGTCATTGTCCA	20																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
----	---	----------------------	----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

TITLE Direct Submission
 JOURNAL Submitted (26-MAR-2003) Medicine, GI/Liver, 2011 Zonal Ave, Los Angeles, CA 90033, USA
 FEATURES
 source 1. 137
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HepG2"
 135. .>137
 /note="BCLX; alternatively spliced"
 /codon_start=1
 /product="BCL2L1"
 /protein_id="AAP22029.1"
 /db_xref="GI:30349285"
 /translation="M"
 CDS
 ORIGIN
 Query Match 100.0%; Score 20; DB 9; Length 137;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCAACCAAGTCATTGTCCA 20
 |||||
 Db 116 CTCAACCAAGTCATTGTCCA 97
 RESULT 5
 AY263336/c
 LOCUS Homo sapiens BCL2L1 mRNA, partial cds, alternatively spliced.
 DEFINITION
 AY263336
 VERSION
 AY263336.1 GI:30349282
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 328)
 Yang, H., Sada, M. and Lu, S.
 5'-alternative splicing of BCLX in HepG2
 Unpublished
 JOURNAL
 REFERENCE
 2 (bases 1 to 328)
 Yang, H., Sada, M. and Lu, S.
 Direct Submission
 TITLE
 Submitted (26-MAR-2003) Medicine, GI/Liver, 2011 Zonal Ave, Los Angeles, CA 90033, USA
 JOURNAL
 FEATURES
 source 1. 328
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HepG2"
 326. .>328
 /note="BCLX; alternatively spliced"
 /codon_start=1
 /product="BCL2L1"
 /protein_id="AAP22028.1"
 /db_xref="GI:30349283"
 /translation="M"
 CDS
 ORIGIN
 Query Match 100.0%; Score 20; DB 9; Length 328;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCAACCAAGTCATTGTCCA 20
 |||||
 Db 307 CTCAACCAAGTCATTGTCCA 288
 RESULT 6
 AY263335/c

LOCUS
 DEFINITION Homo sapiens BCL2L1 mRNA, partial cds, alternatively spliced.
 ACCESSION
 AY263335
 VERSION
 AY263335.1 GI:30349280
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 388)
 Yang, H., Sada, M. and Lu, S.
 5'-alternative splicing of BCLX in HepG2
 Unpublished
 JOURNAL
 REFERENCE
 2 (bases 1 to 388)
 Yang, H., Sada, M. and Lu, S.
 Direct Submission
 TITLE
 Submitted (26-MAR-2003) Medicine, GI/Liver, 2011 Zonal Ave, Los Angeles, CA 90033, USA
 JOURNAL
 FEATURES
 source 1. 388
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HepG2"
 386. .>388
 /note="BCLX; alternatively spliced"
 /codon_start=1
 /product="BCL2L1"
 /protein_id="AAP22027.1"
 /db_xref="GI:30349281"
 /translation="M"
 CDS
 ORIGIN
 Query Match 100.0%; Score 20; DB 9; Length 388;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCAACCAAGTCATTGTCCA 20
 |||||
 Db 367 CTCAACCAAGTCATTGTCCA 348
 RESULT 7
 CQ727769/c
 LOCUS Sequence 13703 from Patent WO02068579.
 DEFINITION
 CQ727769
 ACCESSION
 CQ727769.1 GI:42294740
 VERSION
 CQ727769.1
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1
 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 KITS, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof
 Patent: WO 02068579-A 13703 06-SEP-2002;
 PE Corporation (NY) (US)
 JOURNAL
 FEATURES
 source 1. 512
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 512;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCAACCAAGTCATTGTCCA 20
 |||||

Db 116 CTCACACGATCCATTGTCCA 97

RESULT 8
LOCUS AR054022/c 737 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5834309.
ACCESSION AR054022
VERSION AR054022.1 GI:5978884
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 737)
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.
TITLE Vertebrate apoptosis gene: compositions and methods
JOURNAL Patent: US 5834309-A 8 10-NOV-1998;
FEATURES Location/Qualifiers
source 1..737
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 737;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
|||||
Db 116 CTCACACGATCCATTGTCCA 97

RESULT 11
LOCUS AR371662/c 737 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 7 from patent US 6395510.
ACCESSION AR371662
VERSION AR371662.1 GI:34608659
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 737)
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.
TITLE Vertebrate apoptosis gene: compositions and methods
JOURNAL Patent: US 6395510-A 7 28-MAY-2002;
FEATURES Location/Qualifiers
source 1..737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 737;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
|||||
Db 116 CTCACACGATCCATTGTCCA 97

RESULT 12
LOCUS AR380913/c 737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1458 from patent US 6607879.
ACCESSION AR380913
VERSION AR380913.1 GI:40088547
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 737)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 1458 19-AUG-2003;
FEATURES Location/Qualifiers
source 1..737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 737;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
|||||

Db 116 CTCACACGATCCATTGTCCA 97

RESULT 9
LOCUS AR172595/c 737 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 8 from patent US 6303331.
ACCESSION AR172595
VERSION AR172595.1 GI:17912086
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 737)
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.
TITLE Vertebrate apoptosis gene: compositions and methods
JOURNAL Patent: US 6303331-A 8 16-OCT-2001;
FEATURES Location/Qualifiers
source 1..737
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 737;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
|||||
Db 116 CTCACACGATCCATTGTCCA 97

RESULT 10
LOCUS I52012/c 737 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 7 from patent US 5646008.
ACCESSION I52012
VERSION I52012.1 GI:2473213
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 737)
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.

```
Db      116 CTCACCAAGTCATTGTCCA 97

RESULT 13
HSBCLXS/c
LOCUS      HSBCLXS          737 bp      mRNA      linear      PRI 12-JAN-1995
DEFINITION H. sapiens bcl-xS mRNA.
ACCESSION  Z23116 L20122
VERSION    Z23116.1 GI:623236
KEYWORDS   bcl-xS gene.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 737)
            Direct Submission
            Thompson, C.B.
            Submitted (22-JUN-1993) Craig B Thompson, Howard Hughes Medical
            Institute, University of Chicago, 5841 South Maryland, Chicago, IL,
            60637, USA
REMARK     revised by [3] MAT
REFERENCE  2 (bases 1 to 737)
            Boise, L.H., Gonzalez-Garcia, M., Postema, C.E., Ding, L., Lindsten, T.,
            Turka, L.A., Mao, X., Nunez, G. and Thompson, C.B.
            bcl-x, a bcl-2-related gene that functions as a dominant regulator
            of apoptotic cell death
            Cell 74 (4), 597-608 (1993)
JOURNAL    93364977
MEDLINE    8358789
REFERENCE  3 (bases 1 to 737)
            Thompson, C.B.
            Direct Submission
            Submitted (12-JAN-1995) Craig B Thompson, Howard Hughes Medical
            Institute, University of Chicago, 5841 South Maryland, Chicago, IL,
            60637, USA
COMMENT    On Jan 13, 1995 this sequence version replaced gi:510902.
FEATURES   Location/Qualifiers
            source          1..737
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="bcl-xS"
                        /cell_type="peripheral blood T cell"
                        /dev_stages="Adult"
                        135..647
            gene            /gene="bcl-xS"
            CDS             135..647
                        /gene="bcl-xS"
                        /protein_id="CAA80662.1"
                        /db_xref="GI:623237"
                        /translation="MSOSNRELVDLSYKLSQKGYSMQSDVEENRTAPEETESE
                        NETSAINGNPWSHLADSPVNGATGHSSLDAREVIPMAAVKQALREAGDEFLRYR
                        RAFSDLTSLQHTPTGTAYQSFQVWNLPRDGVNWRIVAFPFGGALCVESVQKEMQ
                        VLGSLSFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 737;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTCACCAAGTCATTGTCCA 20
        |||||
Db      20 CTCACCAAGTCATTGTCCA 1

RESULT 15
AF164517/c
LOCUS      AF164517          766 bp      mRNA      linear      MAM 01-AUG-2000
DEFINITION Ovis aries Bcl-x long protein mRNA, complete cds.
ACCESSION  AF164517
VERSION    AF164517.1 GI:9621785
KEYWORDS   Ovis aries (sheep)
SOURCE     Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Caprinae; Ovis.
REFERENCE  1 (bases 1 to 766)
            Murray, J.F., Dong, Y.B., Leigh, A.J., Scaramuzzi, R.J. and Carter, N.D.
            Bcl-x in the sheep ovary
            Unpublished
REFERENCE  2 (bases 1 to 766)
            Murray, J.F., Dong, Y.B., Leigh, A.J., Scaramuzzi, R.J. and Carter, N.D.
            Direct Submission
            Submitted (01-JUL-1999) Obstetrics and Gynaecology, St. George's
            Hospital Medical School, Cranmer Terrace, London SW17 0RE, UK
FEATURES   Location/Qualifiers
            source          1..766
                        /organism="Ovis aries"
                        /mol_type="mRNA"
                        /db_xref="taxon:9940"
                        /tissue_type="ovary"

Qy      1 CTCACCAAGTCATTGTCCA 20
        |||||
Db      116 CTCACCAAGTCATTGTCCA 97

RESULT 14
RNUI0579/c
LOCUS      RNUI0579          764 bp      DNA      linear      ROD 26-JUN-1994
DEFINITION Rattus norvegicus Bcl-x (bcl-x) gene, complete cds.
ACCESSION  U10579
VERSION    U10579.1 GI:505698
```

CDS
41..742
/note="anti-apoptotic Bcl-2 gene family member; Bcl-x
short protein identified by PCR"
/codon_start=1
/product="Bcl-x long protein"
/protein_id="AAF89532.1"
/db_xref="GI:9621786"
/translation="MSQSNRELIVDFLSYKLSQKGYWSQFSDVEENRTEAPEGTESD
METPSAINGNPSWHLADSPAVNGATGHSRLDAREVIPMAAVKQALREAGDEFEIYYR
RAFSDLTSQLHITPGTAYQSFEQVNVNELFRDGVNMGRIIVAFFSGALCVESVDKEMQ
VLVSRITATWMTYLNLDHLEPWTIQENGWDTFVELYGNNAAESRKQERFNRWFLTGM
TVAGVVLGSLFSRK"

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 766;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCACCACTCCATTGTCCA 20
Db 22 CTCACCACTCCATTGTCCA 3

Search completed: February 4, 2005, 23:30:32
Job time : 485.738 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-1

Perfect score: 20

Sequence: 1 ctcaaccagtcattgtcca 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	136	9 CG608749	CG608749 OST289185
C 2	20	100.0	149	4 BG684338	BG684338 602636083
C 3	20	100.0	151	2 BE386533	BE386533 601273785
C 4	20	100.0	177	2 BF688810	BF688810 602184995
C 5	20	100.0	198	2 BE407849	BE407849 601300889
C 6	20	100.0	200	1 AA351198	AA351198 EST58853
C 7	20	100.0	210	4 BG334446	BG334446 602461986
C 8	20	100.0	213	4 BG478819	BG478819 602525369
C 9	20	100.0	218	4 BG752203	BG752203 602731335
C 10	20	100.0	223	2 BE727284	BE727284 601560967
C 11	20	100.0	225	2 BF026532	BF026532 601672487
C 12	20	100.0	227	2 BE275637	BE275637 601121162
C 13	20	100.0	228	4 BG489250	BG489250 602518262
C 14	20	100.0	230	2 BF685843	BF685843 602143136
C 15	20	100.0	232	4 BG746689	BG746689 602704010
C 16	20	100.0	239	2 BE728507	BE728507 601561960
C 17	20	100.0	248	2 BE386614	BE386614 601273995
C 18	20	100.0	251	4 BM049633	BM049633 603621319
C 19	20	100.0	252	2 BE560320	BE560320 601346468
C 20	20	100.0	254	7 T28063	T28063 EST26052 Hu
C 21	20	100.0	262	4 BG479739	BG479739 602526932
C 22	20	100.0	275	4 BM012517	BM012517 603637151
C 23	20	100.0	287	5 BY236510	BY236510 BY236510
C 24	20	100.0	297	2 BF128036	BF128036 601810793

c 25	20	100.0	301	4 BG419161	BG419161 602445803
c 26	20	100.0	320	5 BY220922	BY220922 BY220922
c 27	20	100.0	322	2 AW125200	AW125200 UI-M-BH2.
c 28	20	100.0	323	5 BY329071	BY329071 BY329071
c 29	20	100.0	325	5 BY191347	BY191347 BY191347
c 30	20	100.0	326	5 BY181507	BY181507 BY181507
c 31	20	100.0	327	5 BY209882	BY209882 BY209882
c 32	20	100.0	336	5 BY219527	BY219527 BY219527
c 33	20	100.0	339	1 AA232598	AA232598 zr28c08.r
c 34	20	100.0	341	5 BY176914	BY176914 BY176914
c 35	20	100.0	343	5 BY333899	BY333899 BY333899
c 36	20	100.0	344	2 BB869154	BB869154 BB869154
c 37	20	100.0	344	5 BY353250	BY353250 BY353250
c 38	20	100.0	348	5 BY010071	BY010071 BY010071
c 39	20	100.0	350	5 BY058101	BY058101 BY058101
c 40	20	100.0	353	5 BY016163	BY016163 BY016163
c 41	20	100.0	355	5 BY180189	BY180189 BY180189
c 42	20	100.0	355	5 BY212491	BY212491 BY212491
c 43	20	100.0	356	5 BY180646	BY180646 BY180646
c 44	20	100.0	356	6 CB813589	CB813589 AMGNNUC:M
c 45	20	100.0	357	2 BB870590	BB870590 BB870590

ALIGNMENTS

RESULT 1
CG608749/c
LOCUS CG608749 136 bp DNA linear GSS 02-OCT-2003
DEFINITION OST289185 Mus musculus 129Sv/Ev Mus musculus genomic clone
OST289185, genomic survey sequence.
ACCESSION CG608749
VERSION CG608749.1 GI:37432598
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 136)
AUTHORS Zambrowicz B.P., Abuin A., Ramirez-Solis R., Richter L.J.,
Piggott J., BeltrandelRio H., Buxton E.C., Edwards J., Finch R.A.,
Fridde C.J., Gupta A., Hansen G., Hu Y., Huang W., Jaing C.,
Key B.W. Jr., Kipp P., Kohnhauff B., Ma Z.-Q., Markesich D.,
Payne R., Potter D.G., Qian L., Shaw J., Schrick J., Shi Z.-Z.,
Sparks M.J., Van Sligtenhorst I., Vogel P., Walke W., Xu N.,
Zhu Q., Person C. and Sands A.T.
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
Location/Qualifiers
1..136
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST289185"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACAGTCATTGTCCA 20

```

Db      98  CTCACCAAGTCATGTGCCA 79
|||||
RESULT 2
BG684338/c
LOCUS      149 bp      mRNA      linear      EST 01-MAY-2001
DEFINITION 602636083F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763900 5',
mRNA sequence.
ACCESSION  BG684338
VERSION     BG684338.1  GI:13915735
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 149)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1620 row: e column: 21
           High quality sequence start: 6
           High quality sequence stop: 122.
           High quality sequence stop: 122.
           Location/Qualifiers
             1..149
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:4763900"
             /tissue_type="primary B-cells from tonsils (cell line)"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH MGC 48"
             /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
             Site 2: EcoRI; cDNA made by oligo-dT priming.
             Directionally cloned into EcoRI/XhoI sites using the
             following 5' adaptor: GGACGAG(G). Size-selected >500bp
             for average insert size 1.8kb. Library constructed by Ling
             Hong in the laboratory of Gerald M. Rubin (University of
             California, Berkeley) using ZAP-cDNA synthesis kit
             (Stratagene) and Superscript II RT (Life Technologies).
             Note: this is a NIH_MGC Library."

FEATURES
source
Query Match      100.0%; Score 20; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  CTCACCAAGTCATGTGCCA 20
|||||
Db  54  CTCACCAAGTCATGTGCCA 35
|||||

RESULT 3
BE386533/c
LOCUS      151 bp      mRNA      linear      EST 21-JUL-2000
DEFINITION 601273785F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614708 5',
mRNA sequence.
ACCESSION  BE386533
VERSION     BE386533.1  GI:9331898
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE  1  (bases 1 to 151)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: ATCC/DCTD/DTP
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
           Plate: LLCM277 row: j column: 21
           High quality sequence stop: 151.
           High quality sequence stop: 151.
           Location/Qualifiers
             1..151
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:3614708"
             /tissue_type="melanotic melanoma"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH MGC 20"
             /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally
             cloned into EcoRI/XhoI sites using the following 5'
             adaptor: GGACGAG(G). Size-selected >500bp for average
             insert size 1.8kb. Library constructed by Ling Hong in
             the laboratory of Gerald M. Rubin (University of
             California, Berkeley) using ZAP-cDNA synthesis kit
             (Stratagene) and Superscript II RT (Life Technologies).".

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  CTCACCAAGTCATGTGCCA 20
|||||
Db  85  CTCACCAAGTCATGTGCCA 66
|||||

RESULT 4
BF688810/c
LOCUS      177 bp      mRNA      linear      EST 22-DEC-2000
DEFINITION 602184955F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299479 5',
mRNA sequence.
ACCESSION  BF688810
VERSION     BF688810.1  GI:11974218
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 177)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM156 row: n column: 24
           High quality sequence start: 2
           High quality sequence stop: 177.
           High quality sequence stop: 177.
           Location/Qualifiers
             1..177
             /organism="Homo sapiens"

```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4299479"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCAAGTCATTGTCCA 20
|||||
Db 91 CTCAACCAAGTCATTGTCCA 72

RESULT 5
BE407849/c
LOCUS      198 bp mRNA linear EST 21-JUL-2000
DEFINITION 601300889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635255 5',
mRNA sequence.
ACCESSION  BE407849
VERSION     BE407849.1 GI:9344299
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 198)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
          Plate: LLCM331 row: b column: 24
          High quality sequence start: 33
          High quality sequence stop: 198.

FEATURES
source
Location/Qualifiers
1..198
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3635255"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 35;

```

```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCAAGTCATTGTCCA 20
|||||
Db 128 CTCAACCAAGTCATTGTCCA 109

RESULT 6
AA351198/c
LOCUS      200 bp mRNA linear EST 21-APR-1997
DEFINITION EST59853 Infant brain Homo sapiens cDNA 5' end similar to apoptosis
regulator bcl-x, mRNA sequence.
ACCESSION  AA351198
VERSION     AA351198.1 GI:2003517
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 200)
AUTHORS   Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.
TITLE     Rapid cDNA sequencing (expressed sequence tags) from a
          directionally cloned human infant brain cDNA library
JOURNAL   Nat. Genet. 4, 373-380 (1993)
MEDLINE   94004965
PUBMED    8401585
COMMENT   Other ESTs: THC105965
          Contact: Kerlavage, AR
          Bioinformatics
          The Institute for Genomic Research
          9712 Medical Center Drive, Rockville, MD 20850 USA
          Tel: 3018699056
          Fax: 3018699423
          Email: arkerlav@tigr.org
          For clone availability, additional sequence and expression
          information related to this EST, please check the TIGR Human Gene
          Index (http://www.tigr.org/cdb/hgi/hgi.html)
          Seq primer: M13 Reverse.

FEATURES
source
Location/Qualifiers
1..200
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):151593"
/dev stage="infant"
/sex="female"
/clone_lib="Infant brain"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI"

ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCAAGTCATTGTCCA 20
|||||
Db 141 CTCAACCAAGTCATTGTCCA 122

RESULT 7
BG334446/c
LOCUS      210 bp mRNA linear EST 27-FEB-2001
DEFINITION 602461986F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4578596 5',
mRNA sequence.
ACCESSION  BG334446
VERSION     BG334446.1 GI:13140884
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 210)

```

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLCMI294 row: 1 column: 21
 High quality sequence stop: 210.

FEATURES

source
 1. .210
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4578596"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 20"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 Query Match 100.0%; Score 20; DB 4; Length 210;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 CTCACACGATCCATTGTCCA 20
 ||||||||||||||||
 DB 124 CTCACACGATCCATTGTCCA 105

RESULT 8
LOCUS BG478819/c 213 bp mRNA linear EST 21-MAR-2001
DEFINITION 60252369F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4643800 5', mRNA sequence.
ACCESSION BG478819 GI:13411098
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 213)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLCMI414 row: 1 column: 17
 High quality sequence stop: 213.

FEATURES

source
 1. .213
 /organism="Homo sapiens"
 /mol_type="mRNA"

/db_xref="taxon:9606"
 /clone="IMAGE:4643800"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 20"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 Query Match 100.0%; Score 20; DB 4; Length 213;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 CTCACACGATCCATTGTCCA 20
 ||||||||||||||||
 DB 127 CTCACACGATCCATTGTCCA 108

RESULT 9

BG752203/c 218 bp mRNA linear EST 15-MAY-2001
LOCUS 602731335F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4874865 5', mRNA sequence.
ACCESSION BG752203
VERSION BG752203.1 GI:14062856
KEYWORDS EST.
SOURCE Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 218)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLCMI755 row: e column: 10
 High quality sequence stop: 218.
 Location/Qualifiers
 1. .218
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4874865"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 43"
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 Note: this is a NIH_MGC Library. |

FEATURES

source
 1. .218
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4874865"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 43"
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 Note: this is a NIH_MGC Library. |

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 218;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

Qy 1 CTCAACCAAGTCATTGTCCA 20
Db 132 CTCAACCAAGTCATTGTCCA 113

RESULT 10
BE727284/c
LOCUS BE727284 223 bp mRNA linear EST 15-SEP-2000
DEFINITION 601560967F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3830416 5',
mRNA sequence.
ACCESSION BE727284
VERSION BE727284.1 GI:10141377
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 223)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM504 row: f column: 17
High quality sequence start: 38
High quality sequence stop: 223.
Location/Qualifiers
FEATURES
source
1..223
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3830416"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match 100.0%; Score 20; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAACCAAGTCATTGTCCA 20
Db 159 CTCACCAAGTCATTGTCCA 140

RESULT 12
BE275637/c
LOCUS BE275637 227 bp mRNA linear EST 13-JUL-2000
DEFINITION 601121162F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988806 5',
mRNA sequence.
ACCESSION BE275637
VERSION BE275637.1 GI:9150595
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 227)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM78 row: k column: 15
High quality sequence start: 27
High quality sequence stop: 227.
Location/Qualifiers
FEATURES
source
1..227
/organism="Homo sapiens"
```

```

Qy 1 CTCAACCAAGTCATTGTCCA 20
Db 157 CTCAACCAAGTCATTGTCCA 138

RESULT 11
BF026532/c
LOCUS BF026532 225 bp mRNA linear EST 10-OCT-2000
DEFINITION 601672487F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955413 5',
mRNA sequence.
ACCESSION BF026532
VERSION BF026532.1 GI:10734244
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 225)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM829 row: n column: 22
High quality sequence start: 40
High quality sequence stop: 225.
Location/Qualifiers
FEATURES
source
1..225
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3955413"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2988806"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/Note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
|||||
Db 161 CTCACACGATCCATTGTCCA 142

RESULT 13
BG489250/c
LOCUS
DEFINITION
602518262F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4636935 5',
mRNA sequence.
ACCESSION
VERSION
BG489250
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 228)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI396 row: k column: 16
High quality sequence stop: 228.
Location/Qualifiers
1..228
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4636935"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
/Note="Organ: lung; Vector: pOTB7; Site:1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
|||||
Db 161 CTCACACGATCCATTGTCCA 142

RESULT 13
BG489250/c
LOCUS
DEFINITION
602518262F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4636935 5',
mRNA sequence.
ACCESSION
VERSION
BG489250
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 228)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI396 row: k column: 16
High quality sequence stop: 228.
Location/Qualifiers
1..228
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4636935"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
/Note="Organ: lung; Vector: pOTB7; Site:1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
|||||
Db 145 CTCACACGATCCATTGTCCA 126

RESULT 14
BF685843/c
LOCUS
DEFINITION
602143136F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304288 5',
mRNA sequence.
ACCESSION
VERSION
BF685843
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 230)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI169 row: g column: 09
High quality sequence stop: 230.
Location/Qualifiers
1..230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4304288"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/Note="Organ: uterus; Vector: pOTB7; Site:1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20
|||||
Db 144 CTCACACGATCCATTGTCCA 125

RESULT 15
BG746689/c
LOCUS
DEFINITION
602704010F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857171 5',
mRNA sequence.
ACCESSION
VERSION
BG746689
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI709 row: d column: 04
High quality sequence stop: 232.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

1. .232
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4857171"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCACCGAGTCCATTGTCCA 20
Db 146 CTCACCGAGTCCATTGTCCA 127

Search completed: February 5, 2005, 08:11:23
Job time : 2391.67 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 480.738 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-2
Perfect score: 20
Sequence: 1 tcccggttgctctgagacat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AR124971
2	20	100.0	20	6	AR144314
3	20	100.0	20	6	BD235150
4	20	100.0	20	6	BD235164
5	20	100.0	20	6	BD235184
6	20	100.0	20	6	BD243061
7	20	100.0	24	6	CQ816672
8	20	100.0	24	6	AX017820
9	20	100.0	24	6	BD137331
10	20	100.0	30	6	AR176180
11	20	100.0	30	6	BD178062
12	20	100.0	30	6	E5260
13	20	100.0	31	6	BD084109
14	20	100.0	31	6	BD102203
15	20	100.0	37	6	AX925704
16	20	100.0	39	6	AR118505
17	20	100.0	512	6	CQ727769
18	20	100.0	513	10	MMU10100
19	20	100.0	513	10	AF136230

c 20	20	100.0	513	10	AF279286
c 21	20	100.0	537	10	S78284
c 22	20	100.0	540	6	AX925690
23	20	100.0	600	6	CQ100639
24	20	100.0	600	6	CQ139631
25	20	100.0	600	6	CQ175964
26	20	100.0	600	6	CQ222399
27	20	100.0	600	6	CQ260961
28	20	100.0	600	6	CQ298444
29	20	100.0	600	6	CQ335104
c 30	20	100.0	600	6	AX925692
c 31	20	100.0	660	6	AX925694
c 32	20	100.0	660	6	AX925696
c 33	20	100.0	699	10	MMBCLXL
c 34	20	100.0	702	4	AY005131
c 35	20	100.0	702	6	BD084108
c 36	20	100.0	702	6	BD102202
c 37	20	100.0	702	9	BT007208
c 38	20	100.0	702	10	MMU10101
c 39	20	100.0	702	12	BT008248
c 40	20	100.0	720	4	AF216205
c 41	20	100.0	723	9	HSU72398
c 42	20	100.0	726	10	RNU34963
c 43	20	100.0	726	10	S76513
c 44	20	100.0	737	6	AR054022
c 45	20	100.0	737	6	AR172595

ALIGNMENTS

RESULT 1
AR124971
LOCUS AR124971 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6172216.
ACCESSION AR124971
VERSION AR124971.1 GI:14110332
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Monia,B.P., Nickoloff,B.J. and Zhang,Q.
TITLE Antisense modulation of BCL-X expression
JOURNAL Patent: US 6172216-A 21 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TCCCGGTTGCTCTGAGACAT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 2
AR144314
LOCUS AR144314 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 42 from patent US 6210892.
ACCESSION AR144314
VERSION AR144314.1 GI:15106181
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Cooke,S.T., Manoharan,M., Wyatt,J.R., Baker,B.F.,

[illegible]

```

PF 11-MAR-1999 JP 2000535770
PR 11-MAR-1998 FR 98/02997
PI FABIEN SCHWEIGHOFFER, LAURENT BRACCO, BRUNO TOCQUE PC
C12Q1/68, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
, C12N15/09, C12N15/09,
PC C12N5/00, C12N15/00, C12N15/00
CC Description of Artificial Sequence: OLIGO
FH Key Location/Qualifiers
FT source 1..24
    /organism='Artificial Sequence'.
FEATURES
    source
        1..24
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
ORIGIN
    Query Match 100.0%; Score 20; DB 6; Length 24;
    Best Local Similarity 100.0%; Pred. No. 3.9;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
    |||||
DB 20 TCCCGGTTGCTCTGAGACAT 1

RESULT 10
AR176180/c
LOCUS AR176180 30 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6310272.
ACCESSION AR176180
VERSION AR176180.1 GI:17917479
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ohashi, Y., Mitsuohara, I. and Malik, K.A.
TITLE Stress resistant plant in which cell death suppressing gene is
introduced and method for producing the same
JOURNAL Patent: US 6310272-A 6 30-OCT-2001;
FEATURES
    source
        1..30
        /organism="unknown"
        /mol_type="unassigned DNA"
ORIGIN
    Query Match 100.0%; Score 20; DB 6; Length 30;
    Best Local Similarity 100.0%; Pred. No. 3.9;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
    |||||
DB 20 TCCCGGTTGCTCTGAGACAT 1

RESULT 11
BD178062/c
LOCUS BD178062 30 bp DNA linear PAT 16-APR-2003
DEFINITION Stress-resistant plant having cell-death inhibitory gene
transferred thereinto and method of constructing the same.
ACCESSION BD178062
VERSION BD178062.1 GI:30015326
KEYWORDS JP 2002300822-A/6.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ohashi, Y., Mitsuohara, I. and Malik, K.A.
TITLE Stress-resistant plant having cell-death inhibitory gene
transferred thereinto and method of constructing the same
JOURNAL Patent: JP 2002300822-A 6 15-OCT-2002;
NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES

```

```

OS Unidentified
PN JP 2002300822-A/6
PD 15-OCT-2002
PF 01-FEB-2002 JP 2002026196
PI YUKO OHASHI, ICHIRO MITSUOHARA, CAMAL A MALIK
PC A01H5/00, C12N15/09//C12N5/10, C12N15/00, C12N5/00 CC Topology:
Linear;
CC Stress-resistant plant having cell-death inhibitory gene CC
transferred
thereinto and method of constructing the same FH Key
Location/Qualifiers
FT source 1..30
    /organism='Unidentified'.
FEATURES
    source
        1..30
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
ORIGIN
    Query Match 100.0%; Score 20; DB 6; Length 30;
    Best Local Similarity 100.0%; Pred. No. 3.9;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
    |||||
DB 20 TCCCGGTTGCTCTGAGACAT 1

RESULT 12
E55260/c
LOCUS E55260 30 bp DNA linear PAT 18-JUN-2001
DEFINITION Stress-tolerant plant having cell death inhibitory gene transferred
thereinto and method for constructing the same.
ACCESSION E55260
VERSION E55260.1 GI:13019329
KEYWORDS JP 2000023583-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Yuko, O., Ichiro, M. and Camal, A.M.
TITLE Stress-tolerant plant having cell death inhibitory gene transferred
thereinto and method for constructing the same
JOURNAL Patent: JP 2000023583-A 6 25-JAN-2000;
NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT OS Artificial Sequence
PN JP 2000023583-A/6
PD 25-JAN-2000
PF 14-JUN-1999 JP 1999167565
PR YUKO OHASHI, ICHIRO MITSUOHARA, CAMAL A MARIKU
PC A01H5/00, A01H1/00, C07H21/04, C07K14/47, C12N5/10, C12N15/09// PC
(C12N5/10, C12R1.91), (C12N15/09, C12R1.91), C12N5/00, C12N15/00, PC
(C12N5/00, C12R1.91), (C12N15/00, C12R1.91)
CC
FH Key Location/Qualifiers
FT source 1..30
    /organism='Artificial Sequence'.
FEATURES
    source
        1..30
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
ORIGIN
    Query Match 100.0%; Score 20; DB 6; Length 30;
    Best Local Similarity 100.0%; Pred. No. 3.9;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
    |||||
DB 20 TCCCGGTTGCTCTGAGACAT 1

```



```
RESULT 13
BD084109/c
LOCUS BD084109 31 bp DNA linear PAT 27-AUG-2002
DEFINITION Method of detecting protein-protein interaction.
ACCESSION BD084109
VERSION BD084109.1 GI:22629719
KEYWORDS JP 2001327296-A/8.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 31)
AUTHORS Kato,S., Eguchi,C. and Nagata,N.
TITLE Method of detecting protein-protein interaction
JOURNAL Patent: JP 2001327296-A 8 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Artificial Sequence
PN JP 2001327296-A/8
PD 27-NOV-2001
PF 24-AUG-2000 JP 2000254418.
PI SEISHI KATO,CHIKASHI EGUCHI,NAOKI NAGATA
PC C12N15/09,C12Q1/02//C07K14/47,(C12N15/09,C12R1:91),(C12Q1/02,
PC C12R1:91)
PC C12N15/00,(C12N15/00,C12R1:91)
CC Synthesized Oligonucleotide
FH Key Location/Qualifiers
FT source 1..31
FT Location/Qualifiers
FEATURES
source 1..31
/molecule="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 30 TCCCGGTTGCTCTGAGACAT 11
|||||
RESULT 14
BD102203/c
LOCUS BD102203 31 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting protein-protein interaction.
ACCESSION BD102203
VERSION BD102203.1 GI:22647777
KEYWORDS WO 0168885-A/8.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 31)
AUTHORS Kato,S., Eguchi,C., Nagata,N. and Otake,M.
TITLE Method for detecting protein-protein interaction
JOURNAL Patent: WO 0168885-A 8 20-SEP-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP,SEISHI KATO,CHIKASHI EGUCHI,NAOKI
NAGATA, MIYAKO OTAKE
COMMENT OS Artificial Sequence
PN WO 0168885-A/8
PD 20-SEP-2001
PF 13-MAR-2001 WO 2001JP001973
PR 15-MAR-2000 JP 00P 073095,24-AUG-2000 JP 00P 254418 PI
SEISHI KATO,CHIKASHI EGUCHI,NAOKI NAGATA,MIYAKO OTAKE PC
C12N15/79,G01N33/68//C12P21/02,C07K19/00
CC Synthesized Oligonucleotide
FH Key Location/Qualifiers
FT source 1..31
FT Location/Qualifiers
FEATURES
source 1..31
/molecule="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 30 TCCCGGTTGCTCTGAGACAT 11
|||||
RESULT 15
AX925704/c
LOCUS AX925704 37 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 19 from Patent WO03083093.
ACCESSION AX925704
VERSION AX925704.1 GI:40244376
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences
REFERENCE 1
AUTHORS Enkel,B., Meents,H. and Fusseneegger,M.
TITLE Host cells having improved cell survival properties and methods to
generate such cells
JOURNAL Patent: WO 03083093-A 19 09-OCT-2003;
Boehringer Ingelheim Pharma GmbH & Co. KG (DE)
FEATURES
source 1..37
/molecule="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide (Eco-Bcl for)"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 36 TCCCGGTTGCTCTGAGACAT 17
|||||
Search completed: February 4, 2005, 23:30:36
Job time : 484.738 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169A-2

Perfect score: 20

Sequence: 1 tcccggtgtctgagacat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003ce:*
- 11: Geneseqn2003de:*
- 12: Geneseqn2004s:*

-Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	Aaz46972 Bcl-Xl mr
2	20	100.0	20	3	Aaz93633 Antisense
3	20	100.0	20	4	Aas15192 Human bcl
4	20	100.0	20	5	Aah27678 Human bcl
5	20	100.0	20	6	Abv73650 Human bcl
6	20	100.0	20	9	Ada24239 Human bcl
7	20	100.0	20	10	Aad64206 Human bcl
8	20	100.0	20	10	Aad64265 Human bcl
9	20	100.0	20	10	Aad64264 Human bcl
10	20	100.0	20	10	Aad64263 Human bcl
11	20	100.0	30	2	Aav57313 5' primer
12	20	100.0	31	5	Aah43465 cDNA clon
13	20	100.0	31	12	Adm45992 Primer 1
14	20	100.0	37	12	Adh52648 RT-PCR pr
15	20	100.0	39	2	Aat40080 Primer fo
16	20	100.0	540	12	Adh52634 Chinese h
17	20	100.0	559	12	ACH73889 Human gen
18	20	100.0	564	12	ACH7595 Human gen
19	20	100.0	600	4	Abag0917 Human foe
20	20	100.0	600	4	Aai40812 Probe #94
21	20	100.0	600	4	Abaz28894 Probe #73

22	20	100.0	600	4	AAK35096
23	20	100.0	600	4	AAK09207
24	20	100.0	600	4	ABs34848 Human liv
25	20	100.0	600	6	ABs09558 Human gen
26	20	100.0	600	12	Adh52636 Chinese h
27	20	100.0	660	12	Adh52638 Chinese h
28	20	100.0	660	12	Adh52640 Chinese h
29	20	100.0	702	5	Aah43464 cDNA clon
30	20	100.0	702	12	Adm45994
31	20	100.0	737	2	AAQ81699
32	20	100.0	737	10	ABz83507 Toxicolog
33	20	100.0	737	11	ADI32132 Human CDN
34	20	100.0	739	12	ADG65218 Human Bcl
35	20	100.0	747	4	AAF30926
36	20	100.0	747	12	ADG65209
37	20	100.0	863	12	ADH52632
38	20	100.0	926	2	AAQ81698
39	20	100.0	926	2	AAT40079
40	20	100.0	926	3	AAZ93614
41	20	100.0	926	4	AAS15189
42	20	100.0	926	4	AAC90810
43	20	100.0	926	6	ABK84766
44	20	100.0	926	8	ABT16641
45	20	100.0	926	10	ADD56779 Human bcl

ALIGNMENTS

RESULT 1

AAZ46972

ID AAZ46972 standard; DNA; 20 BP.

XX AC

XX AC

DT 14-APR-2000 (first entry)

XX Bcl-Xl mRNA specific antisense oligo B.

XX Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;

XX lung; bladder; bcl-2; vascular lesion; antisense; ss.

XX Homo sapiens.

XX WC200001393-A2.

PD 13-JAN-2000.

XX 02-JUL-1999; 99WO-US015250.

XX 02-JUL-1998; 98US-00109614.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Stein CA;

XX WPI; 2000-137140/12.

PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

XX Claim 1; Fig 1; 69pp; English.

CC The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra
CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
CC represent antisense oligos specific for the bcl-X1 mRNA
XX
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 2

AAZ93633

ID AAZ93633 standard; DNA; 20 BP.

XX

AC AAZ93633.

XX

DT 16-AUG-2000 (first entry)

XX

DE Antisense oligonucleotide directed against bcl-x gene.

XX

KW Bcl-x; bcl-xs; antisense; therapy; apoptosis; splice site;
cell signalling molecule; ultraviolet radiation; UV; cancer;
chemotherapy; cytokine; human; ss.

XX

OS Synthetic.

XX

FN WO200020432-A1.

XX

PD 13-APR-2000.

XX

PF 28-SEP-1999; 99WO-US022448.

XX

PR 07-OCT-1998; 98US-00167921.

XX

PR 26-MAR-1999; 99US-00277020.

XX

PR 02-JUN-1999; 99US-00323743.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang Q;

XX

DR WPI; 2000-303730/26.

XX

PT Antisense oligonucleotides targeted to, and capable of inhibiting the

XX

PT expression of, bcl-x nucleic acids, useful for sensitizing cancer cells

XX

PT to apoptotic agents.

XX

PS Claim 3; Page 106; 115pp; English.

XX

CC Antisense inhibition of bcl-x and bcl-xs expression results in apoptosis.
CC Antisense oligonucleotides directed against bcl-x alter the ratio of bcl-
CC x isoforms expressed by a cell or tissue (i.e. increases or decreases the
CC ratio of bcl-x1 to bcl-xs expressed) by altering the splicing of the RNA
CC encoding bcl-x. The antisense oligonucleotide is specifically targeted to
CC a transcript comprising two splice sites which when contacted with the
CC transcript, reduces the relative frequency of splicing at the second
CC splice site so that the resulting ratio of RNA splice products is
CC altered. The use of antisense compounds sensitises cells to the effects
CC of apoptotic stimulants such as a cellular signaling molecule,
CC ultraviolet radiation, a cancer chemotherapeutic drug (e.g. VP-16,
CC cisplatinum or taxol), ceramide (e.g. staurosporine) or a cytokine which
CC causes mitochondrial dysfunction (especially loss of mitochondrial
CC membrane function). The antisense oligonucleotides may have a therapeutic
CC role in the treatment of cancer

XX

SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 3

AAS15192

ID AAS15192 standard; DNA; 20 BP.

XX

AC AAS15192;

XX

DT 16-JAN-2002 (first entry)

XX

DE Human bcl-x antisense oligonucleotide ISIS 15999.

XX

KW Human; antisense oligonucleotide; IL-5R; interleukin-5 receptor; ss;
KW antiinfection; antiinflammatory; cytostatic; inflammation; infection;
KW tumour; ISIS 15999; probe.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "2' methoxyethoxy residues when 16-20 are also 2'
methoxyethoxy residues. All cytosines in this region are
also 5-methyl-cytosine"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2' methoxyethoxy residues when 1-5 are also 2'
methoxyethoxy residues. All cytosines in this region are
also 5-methyl-cytosine"

XX

PN WO200172765-A1.

XX

PD 04-OCT-2001.

XX

PF 28-MAR-2000; 2000WO-US008174.

XX

PR 28-MAR-2000; 2000WO-US008174.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Bennett CF, Crooke ST, Manoharan M, Wyatt JR, Baker BF, Monia BP;

XX

PI Freier SM, McKay R, Karras JG;

XX

DR WPI; 2001-626250/72.

XX

XX Controlling cell behavior, useful e.g. for treatment of tumors, by
PT modulating processing, e.g. splicing, of specific mRNA sequences with non
PT -cleaving antisense agents.

XX

PS Example 14; Page 83; 121pp; English.

XX

CC The invention relates to controlling cell behaviour by modulating the
CC processing of a selected wild-type mRNA target in the cell, is new. The
CC mRNA is bound to a specific-binding antisense compound that does not
CC cleave bound mRNA. The antisense oligonucleotides are useful as research
CC reagents, diagnostic agents (in hybridisation assays), and for treatment
CC or prevention of diseases, e.g. to prevent or delay infections,
CC inflammation and tumours. The present sequence is an antisense
CC oligonucleotide which targets the gene for human bcl-x

XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCCGGTTGCTCTGAGACAT 20
 Db 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 4
 AAH27678
 ID AAH27678 standard; DNA; 20 BP.
 XX
 AC AAH27678;
 XX
 DT 13-AUG-2001 (first entry)
 XX
 DE Human bcl-x antisense chimeric oligonucleotide SEQ ID 21.
 XX
 KW Antisense oligonucleotide; bcl-x; human; apoptosis; inflammation; cancer;
 KW Glioblastoma; leukaemia; autoimmune disorder; Alzheimer's disease;
 KW neurodegenerative disorder; AIDS; Parkinson's disease; phosphorothioate;
 KW ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 PH modified_base 1..20
 FT /mod_base= a
 FT /label= Phosphorothioate internucleotide linkage
 FT modified_base 1..5
 FT /mod_base= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides, where
 FT cytidine residues are 5-methylcytidines"
 FT modified_base 16..20
 FT /mod_base= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides, where
 FT cytidine residues are 5-methylcytidines"
 XX
 PN US2001007025-A1.
 XX
 XX 05-JUL-2001.
 XX
 PF 12-DEC-2000; 2000US-00734846.
 XX
 XX 07-OCT-1998; 98US-00167921.
 PR 26-MAR-1999; 99US-00277020.
 PR 02-JUN-1999; 99US-00233743.
 XX
 XX (BENN/) BENNETT C F.
 PA (DEAN/) DEAN N M.
 PA (MONI/) MONIA B P.
 PA (NICK/) NICKLOFF B J.
 PA (ZHAN/) ZHANG Q Q.
 XX
 PI Bennett CF, Dean NM, Monia BP, Nickloff BJ, Zhang QQ;
 XX
 XX WPI; 2001-397228/42.
 XX
 XX Antisense compound, 8 to 30 nucleobases in length, targeted to a nucleic
 FT acid molecule encoding a human bcl-x, useful for preventing or treating
 FT tumor formation, infection or inflammation.
 FT
 PS Example 16; Page 17; 47pp; English.
 XX
 CC This invention relates to antisense oligonucleotides which are between 8
 CC and 30 nucleobases in length and are targeted to a nucleotide sequence
 CC encoding human bcl-x. Human Bcl-x functions as a bcl-2-independent

CC regulator of apoptosis. The invention includes a method of inhibiting the
 CC expression of bcl-x in human cells or tissues through antisense
 CC inhibition by the antisense oligonucleotides. An antisense compound
 CC containing the oligonucleotide together with a chemotherapeutic agent is
 CC useful for preventing or treating tumour formation. The antisense
 CC compound is also useful for treating or preventing infection or
 CC inflammation. Cancer particularly glioblastoma and leukaemia, autoimmune
 CC disorders and viral infections, AIDS, neurodegenerative disorders like
 CC Alzheimer's or Parkinson's diseases may be treated using compounds
 CC containing the antisense oligonucleotides. The present sequence
 CC represents an antisense oligonucleotide targeted against a region of the
 CC human bcl-x gene
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCCGGTTGCTCTGAGACAT 20
 Db 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 5
 ABV73650
 ID ABV73650 standard; DNA; 20 BP.
 XX
 AC ABV73650;
 XX
 DT 06-JAN-2003 (first entry)
 XX
 DE Human bcl-x exon 1/exon 2 antisense oligonucleotide #SEQ ID 42.
 XX
 KW Antisense therapy; antisense oligonucleotide; apoptosis; mitosis;
 KW differentiation; stress; hormone; cytokine; signalling molecule;
 KW mRNA modulation; mRNA cleavage; therapeutic; human; bcl-x; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 PH modified_base 1..20
 FT /mod_base= a
 FT /mod_base= OTHER
 FT /note= "nucleotides 1-5 and 16-20 are 2'-methoxyethoxy
 FT (2'-MOE); all 2'-MOE cytosines are 5-methyl-cytosines; all
 FT linkages are phosphorothioate"
 XX
 PN US2002049173-A1.
 XX
 XX 25-APR-2002.
 XX
 PF 12-DEC-2000; 2000US-00734847.
 XX
 XX 26-MAR-1999; 99US-00277020.
 PR
 PR (BENN/) BENNETT C F.
 PA (CROO/) CROOKE S T.
 PA (MANO/) MANOHARAN M.
 PA (WYAT/) WYATT J.
 PA (BAKE/) BAKER B F.
 PA (MONI/) MONIA B P.
 PA (MCKA/) MCKAY R.
 PA (KARR/) KARRAS J G.
 XX
 PI Bennett CF, Crooke ST, Manoharan M, Wyatt J, Baker BF, Monia BP;
 PI McKay R, Karras JG;
 PI WPI; 2002-415043/44.
 DR
 XX Controlling cell behavior by modulating mRNA modification, useful in
 PT therapeutics and as research tool, comprises using antisense
 PT oligonucleotide which hybridize to mRNA and block modification regions

```

PT such as splice acceptor sites.
XX
PS Example 14; Page 28; 50pp; English.
XX
CC The invention relates to the control of cell behaviour by modulating the
CC processing of a wild-type mRNA target, comprising binding to the target
CC an antisense compound which specifically hybridises to the target and
CC does not elicit cleavage of the mRNA upon binding. The method of the
CC invention can be used in therapeutics (i.e antisense therapy), including
CC prophylaxis, and as a research tool. It is used for controlling the
CC behaviour of a cell (especially responses such as apoptosis, mitosis,
CC differentiation and quiescence to stimuli such as stress, hormones,
CC cytokines and other signalling molecules), tissue or organism through
CC antisense modulation of mRNA processing. The current sequence represents
CC a human bcl-x exon 1/exon 2 antisense oligonucleotide designated SEQ ID
CC 42, designed to target areas of exon 1 and exon 2 of human bcl-x,
CC particularly around the exon 1/exon 2 splice site and in sequence regions
CC present in bcl-x1 but not bcl-xs
XX
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
DB 1 TCCCGGTTGCTCTGAGACAT 20
RESULT 6
ADA24239
ID ADA24239 standard; DNA; 20 BP.
AC
AC ADA24239;
XX
XX 20-NOV-2003 (first entry)
DE Human bcl-x1 antisense oligonucleotide MB-006 SEQ ID NO:22.
XX
XX therapeutic oligonucleotide; double-stranded RNA; dsRNA; mobile protein;
KW cytostatic; immunosuppressive; virucide; anti-HIV; antibacterial;
KW cardiant; hyperproliferation; cancer; haematological; metastatic;
KW autoimmune disease; infection; endocrine; neural; cardiovascular;
KW pulmonary; reproductive system disorder; endocytosis; metabolic process;
KW murine; intracellular adhesion molecule 1; ICAM-1;
KW antisense oligonucleotide; phosphorothioate; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
XX WO2003069306-A2.
XX
XX 21-AUG-2003.
XX
XX 13-FEB-2003; 2003WO-US004323.
XX
XX 13-FEB-2002; 2002US-0356053P.
XX
XX (MEDB-) MEDBRIDGE INC.
XX
XX Xie D;
XX
XX WPI; 2003-646491/61.
DR
XX Treating diseases with oligonucleotides or interfering RNA, useful e.g.
XX for cancer or autoimmune diseases, covalently coupled to mobile proteins,
PT

```

```

PT in vivo or in vitro.
XX
PS Claim 128; Page 12; 42pp; English.
XX
CC The present invention describes a method for treating a disease by
CC administering: (a) a therapeutic oligonucleotide (TON) or double-stranded
CC RNA (dsRNA) that includes a reactive group (RG) that can react with a
CC mobile protein (MP) to form a covalent conjugate of TON/dsRNA and MP; or
CC (b) TON or dsRNA already conjugated to MP through a covalent bond. Also
CC described: (1) TON of 15-30 bases that includes (i) a part that binds to
CC target RNA or DNA and (ii) RG; (2) TON of 15-30 bases that includes a
CC part that binds to target RNA or DNA and is conjugated to MP through a
CC covalent link; (3) dsRNA that includes RG; and (4) dsRNA that is
CC conjugated to MP through a covalent link. TON have cytostatic,
CC immunosuppressive, virucide, anti-HIV, antibacterial and cardiant
CC activities. The method is used to treat, or prevent, hyperproliferation
CC (particularly cancers, solid or haematological, including prevention of
CC metastatic spread); autoimmune diseases; viral or bacterial infections;
CC endocrine, neural, cardiovascular, pulmonary or reproductive system
CC disorders. Also where TON or dsRNA are labelled, they can be used for
CC diagnosis and monitoring of therapy. When linked to a mobile protein,
CC TON/dsRNA have better cell entry (via endocytosis or other parts of the
CC mobile protein metabolic process) and longer therapeutic life, increased
CC from hours to weeks (the result of increased resistance to nuclease),
CC without loss of affinity for the target. In many cases immune response to
CC TON/dsRNA is also reduced, as is non-specific binding to endogenous
CC proteins. The present sequence represents a human bcl-x1 antisense
CC oligonucleotide, which is a specifically claimed TON from the present
CC invention.
XX
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
DB 1 TCCCGGTTGCTCTGAGACAT 20
RESULT 7
ADA64206
ID ADA64206 standard; DNA; 20 BP.
XX
AC ADA64206;
XX
XX 12-FEB-2004 (first entry)
DE Human bcl-x antisense oligonucleotide ISIS #15999.
XX
XX Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;
KW retinitis pigmentosa; myocardial infarction; neuroprotective; cytostatic;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW acquired immune deficiency syndrome; neurodegenerative disorder; AIDS;
KW neurotropic; anticonvulsant; vasotropic; therapy; cerebroprotective;
KW stroke; antisense; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
FT cytidines are 5-methyl cytidines"
FT modified_base 16..20
FT /*tag= c
FT

```

```

FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
FT      cytidines are 5-methyl cytidines"
FN      US2003191300-A1.
PD      09-OCT-2003.
XX
XX      21-NOV-2002; 2002US-00302262.
XX
XX      07-OCT-1998; 98US-00167921.
XX      26-MAR-1999; 99US-00277020.
XX      02-JUN-1999; 99US-00323743.
XX      12-DEC-2000; 2000US-00734846.
XX
XX      (BENN/) BENNETT C F.
XX      (DEAN/) DEAN N M.
XX      (MONI/) MONIA B P.
XX      (NICK/) NICKOLOFF B J.
XX      (ZHAN/) ZHANG Q Q.
XX
XX      Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;
XX      WPI; 2003-864192/80.
XX
XX      Compound useful for treating reduced apoptotic conditions e.g. cancer
XX      comprises nucleobases targeted to nucleic acid molecule encoding human
XX      gene encoding intracellular membrane protein.
XX
XX      Example 18; SEQ ID NO 21; Opp; English.
XX
XX      The present invention relates to methods for modulating the expression of
XX      bcl-x. The invention is useful for sensitising cancer cells such as
XX      glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet
XX      radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention
XX      is useful for treating acquired immune deficiency syndrome (AIDS),
XX      neurodegenerative disorders such as Alzheimer's disease, Parkinson's
XX      disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy
XX      and ischaemia such as myocardial infarction and stroke. The present
XX      sequence is human bcl-x antisense oligonucleotide
XX
XX      Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 20; DB 10; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.7;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 TCCCGGTTGCTCTGAGACAT 20
XX      |||||
XX      1 TCCCGGTTGCTCTGAGACAT 20

RESULT 8
AAD64265
ID      AAD64265 standard; DNA; 20 BP.
XX
XX      AAD64265;
XX
XX      12-FEB-2004 (first entry)
XX
XX      Human bcl-x antisense oligonucleotide ISIS #17959.
XX
XX      Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;
XX      retinitis pigmentosa; myocardial infarction; neuroprotective; cytostatic;
XX      Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX      acquired immune deficiency syndrome; neurodegenerative disorder; AIDS;
XX      nontropic; anticonvulsant; vasotropic; therapy; cerebroprotective;
XX      stroke; antisense; phosphorothioate backbone; ss.
XX
XX      Homo sapiens.
XX      Synthetic.
XX
XX      Key      Location/Qualifiers

```

```

FT      modified_base 1. 20
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone"
FN      modified_base 11. 20
FN      /*tag= b
FN      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
FT      cytosines are 5-methyl cytosines (5mec)"
XX
XX      US2003191300-A1.
XX
XX      09-OCT-2003.
XX
XX      21-NOV-2002; 2002US-00302262.
XX
XX      07-OCT-1998; 98US-00167921.
XX      26-MAR-1999; 99US-00277020.
XX      02-JUN-1999; 99US-00323743.
XX      12-DEC-2000; 2000US-00734846.
XX
XX      (BENN/) BENNETT C F.
XX      (DEAN/) DEAN N M.
XX      (MONI/) MONIA B P.
XX      (NICK/) NICKOLOFF B J.
XX      (ZHAN/) ZHANG Q Q.
XX
XX      Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;
XX      WPI; 2003-864192/80.
XX
XX      Compound useful for treating reduced apoptotic conditions e.g. cancer
XX      comprises nucleobases targeted to nucleic acid molecule encoding human
XX      gene encoding intracellular membrane protein.
XX
XX      Example 21; Page 19; Opp; English.
XX
XX      The present invention relates to methods for modulating the expression of
XX      bcl-x. The invention is useful for sensitising cancer cells such as
XX      glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet
XX      radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention
XX      is useful for treating acquired immune deficiency syndrome (AIDS),
XX      neurodegenerative disorders such as Alzheimer's disease, Parkinson's
XX      disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy
XX      and ischaemia such as myocardial infarction and stroke. The present
XX      sequence is human bcl-x antisense oligonucleotide. This sequence is the
XX      analogue of ISIS 15999
XX
XX      Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 20; DB 10; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.7;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 TCCCGGTTGCTCTGAGACAT 20
XX      |||||
XX      1 TCCCGGTTGCTCTGAGACAT 20

RESULT 9
AAD64264
ID      AAD64264 standard; DNA; 20 BP.
XX
XX      AAD64264;
XX
XX      12-FEB-2004 (first entry)
XX
XX      Human bcl-x antisense oligonucleotide ISIS #17958.
XX
XX      Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;
XX      retinitis pigmentosa; myocardial infarction; neuroprotective; cytostatic;
XX      Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX      acquired immune deficiency syndrome; neurodegenerative disorder; AIDS;

```

KW nootropic; anticonvulsant; vasotropic; therapy; cerebroprotective;
 KW stroke; antisense; phosphorothioate backbone; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20 /tag= a
 FT /mod_base= OTHER
 FT modified_base 1..10 /note= "Phosphorothioate backbone"
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
 FT cytosines are 5-methyl cytosines (5mC)"
 XX
 PN US2003191300-A1.
 XX
 XX
 PD 09-OCT-2003.
 XX
 XX 21-NOV-2002; 2002US-00302262.
 XX
 XX 07-OCT-1998; 98US-00167921.
 PR 26-MAR-1999; 99US-00277020.
 PR 02-JUN-1999; 99US-00323743.
 PR 12-DEC-2000; 2000US-00734846.
 XX
 PA (BENN/) BENNETT C F.
 PA (DEAN/) DEAN N M.
 PA (MONI/) MONIA B P.
 PA (NICK/) NICKOLOFF B J.
 PA (ZHAN/) ZHANG Q Q.
 XX
 XX Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;
 XX WPI; 2003-864192/80.
 XX
 XX Compound useful for treating reduced apoptotic conditions e.g. cancer
 FT comprises nucleobases targeted to nucleic acid molecule encoding human
 FT gene encoding intracellular membrane protein.
 XX
 XX Example 21; Page 19; Opp; English.
 XX
 CC The present invention relates to methods for modulating the expression of
 CC bcl-x. The invention is useful for sensitising cancer cells such as
 CC glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet
 CC radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention
 CC is useful for treating acquired immune deficiency syndrome (AIDS),
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy
 CC and ischaemia such as myocardial infarction and stroke. The present
 CC sequence is human bcl-x antisense oligonucleotide. This sequence is the
 CC analogue of ISIS 15999
 XX
 XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 20; DB 10; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 1.7;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TCCCGGTTGCTTGACAT 20
 DB 1 TCCCGGTTGCTTGACAT 20
 RESULT 10
 AAD64263
 ID AAD64263 standard; DNA; 20 BP.
 XX
 AC AAD64263;
 XX
 DT 12-FEB-2004 (first entry)

XX
 DE Human bcl-x antisense oligonucleotide ISIS #17791.
 XX
 KW Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;
 KW retinitis pigmentosa; myocardial infarction; neuroprotective; cytoskeletal;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW acquired immune deficiency syndrome; neurodegenerative disorder; AIDS;
 KW nootropic; anticonvulsant; vasotropic; therapy; cerebroprotective;
 KW stroke; antisense; phosphorothioate backbone; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..5 /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
 FT cytosines are 5-methyl cytosines (5mC)"
 FT modified_base 5..16 /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 16..20 /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
 FT cytosines are 5-methyl cytosines (5mC)"
 XX
 PN US2003191300-A1.
 XX
 XX 09-OCT-2003.
 XX
 XX 21-NOV-2002; 2002US-00302262.
 XX
 XX 07-OCT-1998; 98US-00167921.
 PR 26-MAR-1999; 99US-00277020.
 PR 02-JUN-1999; 99US-00323743.
 PR 12-DEC-2000; 2000US-00734846.
 XX
 PA (BENN/) BENNETT C F.
 PA (DEAN/) DEAN N M.
 PA (MONI/) MONIA B P.
 PA (NICK/) NICKOLOFF B J.
 PA (ZHAN/) ZHANG Q Q.
 XX
 XX Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;
 XX WPI; 2003-864192/80.
 XX
 XX Compound useful for treating reduced apoptotic conditions e.g. cancer
 FT comprises nucleobases targeted to nucleic acid molecule encoding human
 FT gene encoding intracellular membrane protein.
 XX
 XX Example 21; Page 19; Opp; English.
 XX
 CC The present invention relates to methods for modulating the expression of
 CC bcl-x. The invention is useful for sensitising cancer cells such as
 CC glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet
 CC radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention
 CC is useful for treating acquired immune deficiency syndrome (AIDS),
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy
 CC and ischaemia such as myocardial infarction and stroke. The present
 CC sequence is human bcl-x antisense oligonucleotide. This sequence is the
 CC analogue of ISIS 15999
 XX
 XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 20; DB 10; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 1.7;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20
| | | | |
Db 1 TCCCGGTGCTCTGAGACAT 20
| | | | |
RESULT 11
AAV57313/C
ID AAV57313 standard; DNA; 30 BP.
XX AC AAV57313;
XX DT 19-NOV-1998 (first entry)
XX DE 5' primer, used to amplify bcl-xL cDNA.
XX KW Primer; PCR; amplification; bcl-xL; cell death suppressing gene; pM21;
XX KW pBluescript; stress-resistant plant; UV irradiation; high salinity;
XX KW superoxide-generating herbicide; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN EP864650-A2.
XX PD 16-SEP-1998.
XX PF 11-MAR-1998; 98EP-00301786.
XX PR 11-MAR-1997; 97JP-00056743.
XX PR 19-JAN-1998; 98JP-00080856.
XX PA (NOR) NAT INST AGROBIOLOGICAL RESOURCES MIN.
XX PI Ohashi Y, Mitsuhashi I, Malik KA;
XX DR WPI; 1998-469234/41.
XX PT New stress-resistant transgenic plants, comprise cell death suppressing
PT gene - used to confer resistance to stress caused by UV irradiation,
PT super-oxide-generating herbicides or high salinity.
XX PS Example 2; Page 7; 31pp; English.
XX CC Primers AAV57313 and AAV57314 were used to amplify the human bcl-xL (cell
CC death suppressing gene) gene isolated from a human cDNA library. After
CC amplification, the product was cloned into the EcoRI site of pBluescript,
CC thus obtaining the plasmid pM21. This plasmid, was used in the
CC construction of an expression vector which can then be used in the
CC preparation of a stress-resistant plant, by introducing this gene into a
CC plant cell and then using this cell to regenerate a plant. The stress-
CC resistant plants produced by this method have been found to show
CC increased resistance to stress caused by UV irradiation, superoxide-
CC generating herbicides or high salinity
XX SQ Sequence 30 BP; 6 A; 6 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCCGGTGCTCTGAGACAT 20
| | | | |
Db 20 TCCCGGTGCTCTGAGACAT 1
| | | | |
RESULT 12
AAH43465/C
ID AAH43465 standard; DNA; 31 BP.;
XX AC AAH43465;
XX DT 04-DEC-2001 (first entry)
XX DE
XX PF 24-JUN-2002; 2002JP-00183456.
cDNA clone HP03564 ORF, primer P1.
Nw38; NwBP; protein interaction; reporter function; eukaryotic cell;
localization; protein network; intracellular; primer; amplify; PCR;
polymerase chain reaction; mitochondria; ss.
Synthetic.
WO200168885-A1.
20-SEP-2001.
13-MAR-2001; 2001WO-JP001973.
15-MAR-2000; 2000JP-00073095.
24-AUG-2000; 2000JP-00254418.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
Kato S, Eguchi C, Nagata N, Otake M;
WPI; 2001-590069/66.
Detection of protein-protein interactions for screening compounds capable
of modifying the interaction comprises observing intracellular
localization of one protein after altering the modification pattern.
Example 6; Page 30; 33pp; Japanese.
The sequences given in AAH43465-67 are primers which were used to amplify
the open reading frame of the mitochondrial cDNA clone HP03564. The
protein encoded by the amplified sequence was used in the method of the
invention. The method allows detection of interactions between a protein
X and a protein Y which has a reporter function in eukaryotic cells, and
comprises modifying the localization patterns of X and/or Y, and the
localization of Y in the cell is observed using the reporter function.
This method is useful for the elucidation of protein networks within the
cell. It is also applicable for the discovery of new proteins and low-
molecular drugs, by observing their effect on intracellular protein
interactions
SQ Sequence 31 BP; 8 A; 8 C; 11 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 5; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCCGGTGCTCTGAGACAT 20
| | | | |
Db 30 TCCCGGTGCTCTGAGACAT 11
| | | | |
RESULT 13
ADM45992/C
ID ADM45992 standard; DNA; 31 BP.
XX AC ADM45992;
XX DT 03-JUN-2004 (first entry)
XX DE
XX KW random oligonucleotide library; protein interaction; ligand;
KW receptor binding site; PCR; primer; ss; human;
KW apoptosis inhibitory factor; Bcl-XL.
XX OS Homo sapiens.
XX PN JP2004024078-A.
XX PD 29-JAN-2004.
XX PF 24-JUN-2002; 2002JP-00183456.

XX 24-JUN-2002; 2002JP-00183456.
 XX (SERE-) SERESUTA REKISHIKO SCI KK.
 XX WPI; 2004-161478/16.
 XX Random oligonucleotide useful for detecting protein interaction, having
 PT base sequence, where each base of 1st and 2nd of the codon is the any of
 PT G, C,T (U), or A and the base of 3rd of codon is G or C, or G or T (U).
 XX Example 2; SEQ ID NO 1; 43pp; Japanese.
 XX The invention relates to a novel random oligonucleotide having a base
 CC sequence where each base of the 1st and 2nd codon is any of G, C, T (U)
 CC or A and each base of the 3rd codon is G or C, or G or T (U). The methods
 CC of the invention may be useful for preparing a random oligonucleotide
 CC preparation to be used for detecting protein interactions or for
 CC screening ligand or receptor protein binding sites. The current sequence
 CC is that of the PCR primer 1 of the invention which was used to amplify
 CC human apoptosis inhibitory factor Bcl-XL cDNA.
 XX
 SQ Sequence 31 BP; 7 A; 10 C; 11 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 12; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCCGGTGCTCTGAGACAT 20
 Db 29 TCCCGGTGCTCTGAGACAT 10
 RESULT 14
 ADH52648/c
 ID ADH52648 standard; DNA; 37 BP.
 XX
 AC ADH52648;
 XX
 DT 25-MAR-2004 (first entry)
 DE RT-PCR primer Eco-Bcl used to amplify Chinese hamster bcl-xL RNA.
 XX
 XX mammalian myeloma host cell; protein production; anti-apoptosis;
 KW cell death; Chinese hamster; bcl-xL; PCR; primer; ss; RT-PCR.
 XX
 OS Synthetic.
 OS Cricetulus griseus.
 XX
 PN US2003219871-A1.
 XX
 PD 27-NOV-2003.
 XX
 PF 28-MAR-2003; 2003US-00402017.
 XX
 PR 02-APR-2002; 2002US-0369307P.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
 XX
 PI Enkel B, Meents H, Fussenegger M;
 XX
 DR WPI; 2004-033642/03.
 XX
 PT New genetically engineered hamster or murine myeloma host cells
 PT comprising enhanced levels of active anti-apoptosis genes, useful for
 PT producing complex protein therapeutics.
 XX
 PS Example 5; SEQ ID NO 19; 46pp; English.
 XX
 CC The invention relates to a novel mammalian host cell for producing
 CC protein therapeutics. The host cell comprises a hamster or a murine
 CC myeloma cell that is genetically modified by introduction of nucleic acid
 CC sequences encoding an anti-apoptosis gene, a selectable amplifiable

CC marker gene and at least one gene of interest. The host cell of the
 CC invention may be useful for producing at least one protein encoded by a
 CC gene of interest. The DNA, polypeptide and the methods may be used for
 CC inhibiting or delaying cell death. The current sequence is that of the
 CC Chinese hamster anti-apoptosis bcl-xL-related PCR primer which was used
 CC in the exemplification of the invention.
 XX
 SQ Sequence 37 BP; 9 A; 12 C; 10 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 12; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCCGGTGCTCTGAGACAT 20
 Db 36 TCCCGGTGCTCTGAGACAT 17
 RESULT 15
 AAT40080/c
 ID AAT40080 standard; cDNA; 39 BP.
 XX
 AC AAT40080;
 XX
 DT 30-MAR-1997 (first entry)
 XX
 DE Primer for bcl-XS open reading frame amplification by PCR.
 XX
 KW Primer; bcl-XS; PCR; polymerase chain reaction; bcl-XL; T-lymphocyte;
 KW activation; cell death; antibody; CD28 costimulation; gene therapy; HIV;
 KW AIDS; antisense; immune disorder; autoimmune disease; graft rejection;
 KW graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO9634956-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 02-MAY-1996; 96WO-US006203.
 XX
 PR 04-MAY-1995; 95US-00435518.
 PR 07-JUN-1995; 95US-00481739.
 XX
 PA (USNA) US SEC OF NAVY.
 PA (ARCH-) ARCH DEV CORP.
 XX
 PI June CH, Thompson CB;
 XX
 DR WPI; 1996-506159/50.
 XX
 PT Inducing or preventing death of T cells by bcl-XL protein regulation -
 PT used to increase survival of HIV infected cells or to down-regulate
 PT immune responses in immune diseases.
 XX
 PS Example 5; Page 38; 76pp; English.
 XX
 CC This primer may be used with AAT40081 in PCR to amplify the bcl-XS (short
 CC form splice variant) open reading frame in the bcl-X gene, which also
 CC encodes a long form (bcl-XL) protein. Bcl-XL protein protects T-
 CC lymphocytes against cell death, and bcl-XS is a dominant regulator. The
 CC amplified bcl-XS fragment has been cloned into NdeI and BamHI sites of
 CC plasmid pBT-3b, and expressed in BL21 cells, for use in generation of
 CC rabbit polyclonal antibodies and mouse monoclonal antibodies to monitor
 CC bcl-XL and bcl-XS protein levels in T-cells. Immunoassays using the
 CC antibodies have shown that resting T-cells do not express bcl-XL, whereas
 CC anti-CD3- activated T-cells express the protein, and expression levels
 CC are increased by anti-CD28 costimulation. The bcl-XL gene may be
 CC introduced into T-cells in vivo or ex vivo for HIV infection gene
 CC therapy, or may be introduced in antisense orientation for gene therapy
 CC of autoimmune disease, graft rejection or graft-versus-host disease
 XX
 SQ Sequence 39 BP; 11 A; 7 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20
 |||||
 Db 32 TCCCGGTGCTCTGAGACAT 13

Search completed: February 4, 2005, 21:52:37
 Job time : 260.033 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-2

Perfect score: 20

Sequence: 1 tcccggtgtctgagacat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsl1:*
9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	119	2	BE796096
C 2	20	100.0	129	2	BE275197
C 3	20	100.0	136	9	CG608749
C 4	20	100.0	151	2	BE386533
C 5	20	100.0	162	4	BM050693
C 6	20	100.0	177	2	BF688810
C 7	20	100.0	200	1	AA351198
C 8	20	100.0	210	4	BG334446
C 9	20	100.0	213	4	BG478819
C 10	20	100.0	218	4	BG752203
C 11	20	100.0	223	2	BF027284
C 12	20	100.0	225	2	BF026532
C 13	20	100.0	227	2	BE275637
C 14	20	100.0	230	2	BF685843
C 15	20	100.0	232	4	BG746689
C 16	20	100.0	239	2	BE728507
C 17	20	100.0	248	2	BE386614
C 18	20	100.0	251	2	BE269450
C 19	20	100.0	251	4	BM049633
C 20	20	100.0	252	2	BE560320
C 21	20	100.0	262	4	BG479739
C 22	20	100.0	275	4	BM012517
C 23	20	100.0	297	2	BF128036
C 24	20	100.0	301	4	BG419161

C 25	20	100.0	320	5	BY220922
C 26	20	100.0	323	5	BY329071
C 27	20	100.0	325	5	BY191347
C 28	20	100.0	326	5	BY181507
C 29	20	100.0	327	5	BY209882
C 30	20	100.0	336	5	BY219527
C 31	20	100.0	341	5	BY176914
C 32	20	100.0	344	2	BB869154
C 33	20	100.0	348	5	BY010071
C 34	20	100.0	350	5	BY058101
C 35	20	100.0	353	5	BY016163
C 36	20	100.0	355	5	BY180189
C 37	20	100.0	355	5	BY212491
C 38	20	100.0	356	5	BY180646
C 39	20	100.0	356	6	CB813589
C 40	20	100.0	357	2	BB870590
C 41	20	100.0	358	5	BY203613
C 42	20	100.0	361	5	BY176753
C 43	20	100.0	363	5	BY221240
C 44	20	100.0	363	5	BY293078
C 45	20	100.0	367	2	BB843018

ALIGNMENTS

RESULT 1
BE796096/c
LOCUS BE796096 119 bp mRNA linear EST 20-SEP-2000
DEFINITION 601590910F1 NIH_MGC_7 Homo sapiens CDNA clone IMAGE:3944786 5', mRNA sequence.
ACCESSION BE796096
VERSION BE796096.1 GI:10217294
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 119)
NTH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-x@mail.nih.gov
Tissue Procurement: DCTD/DTp
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM802 row: d column: 03
High quality sequence start: 25
High quality sequence stop: 119.
Location/Qualifiers
1. 119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3944786"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES

source

ORIGIN


```

/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN
 Query Match 100.0%; Score 20; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20
 |||||
Db 123 TCCCGGTGCTCTGAGACAT 104

RESULT 5
BM050693/c
LOCUS BM050693 162 bp mRNA linear EST 07-NOV-2001
DEFINITION 603633458F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5423943 5',
 mRNA sequence.
ACCESSION BM050693
VERSION BM050693.1 GI:16779960
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 162)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LUCM1884 row: c column: 16
 High quality sequence stop: 162.
 Location/Qualifiers
 1..162
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5423943"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_43"
 /notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 20; DB 4; Length 162;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20

Db 114 TCCCGGTGCTCTGAGACAT 95
 |||||
RESULT 6
BF688810/c
LOCUS BF688810 177 bp mRNA linear EST 22-DEC-2000
DEFINITION 602184995F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299479 5',
 mRNA sequence.
ACCESSION BF688810
VERSION BF688810.1 GI:11974218
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 177)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LUCM1156 row: n column: 24
 High quality sequence start: 2
 High quality sequence stop: 177.
 Location/Qualifiers
 1..177
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4299479"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_43"
 /notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 20; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20
 |||||
Db 129 TCCCGGTGCTCTGAGACAT 110

RESULT 7
AA351198/c
LOCUS AA351198 200 bp mRNA linear EST 21-APR-1997
DEFINITION EST58853 Infant brain Homo sapiens cDNA 5' end similar to apoptosis
 regulator bcl-x, mRNA sequence.
ACCESSION AA351198
VERSION AA351198.1 GI:2003517
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
 1 (bases 1 to 200)

AUTHORS. Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.
TITLE Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library
JOURNAL Nat. Genet. 4, 373-380 (1993)
MEDLINE 94004965
PUBMED 8401585
COMMENT Other ESTs: THC105965
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES source
 Location/Qualifiers
 1..200
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):151593"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="infant"
 /clone_lib="Infant brain"
 /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI"

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 200;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20
 |||||
 Db 179 TCCCGGTTGCTCTGAGACAT 160

RESULT 8
BG334446/c
LOCUS BG334446 210 bp mRNA linear EST 27-FEB-2001
DEFINITION 602461986F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4578596 5', mRNA sequence.

ACCESSION BG334446
VERSION BG334446.1 GI:13140884
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 210)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLCM1294 row: 1 column: 21
 High quality sequence stop: 210.
 Location/Qualifiers
 1..210
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4578596"

FEATURES

source
 Location/Qualifiers
 1..210
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4578596"

/tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_20"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 210;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20
 |||||
 Db 162 TCCCGGTTGCTCTGAGACAT 143

RESULT 9
BG478819/c
LOCUS BG478819 213 bp mRNA linear EST 21-MAR-2001
DEFINITION 602525369F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4643800 5', mRNA sequence.

ACCESSION BG478819
VERSION BG478819.1 GI:13411098
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 213)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLCM1414 row: 1 column: 17
 High quality sequence stop: 213.
 Location/Qualifiers
 1..213
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4643800"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_20"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES

source
 Location/Qualifiers
 1..213
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4643800"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_20"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 213;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20


```

Db      165  TCCCGGTGCTCTGAGACAT 146
|||||
RESULT 10
BG752203/c
LOCUS   602731335F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4874865 5',
DEFINITION mRNA sequence.
ACCESSION BG752203
VERSION   BG752203.1 GI:14062856
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 218)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-re@mail.nih.gov
        Tissue Procurement: ATCC
        CDNA Library Preparation: Ling Hong/Rubin Laboratory
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: LLCM1755 row: e column: 10
        High quality sequence stop: 218.
FEATURES             source
    Location/Qualifiers
        1..218
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:4874865"
        /tissue_type="normal pigmented retinal epithelium"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC_43"
        /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
        EcoRI; cDNA made by oligo-dT priming. Directionally
        cloned into EcoRI/XhoI sites using the following 5'
        adaptor: GGCACGAG(G). Library constructed by Ling Hong
        in the laboratory of Gerald M. Rubin (University of
        California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies).
        Note: this is a NIH_MGC Library. |"
ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  TCCCGGTGCTCTGAGACAT 20
      |||||||
Db   170 TCCCGGTGCTCTGAGACAT 151

RESULT 11
BE727284/c
LOCUS   601560967F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3830416 5',
DEFINITION mRNA sequence.
ACCESSION BE727284
VERSION   BE727284.1 GI:10141377
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 223)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.

```

```

TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-re@mail.nih.gov
        Tissue Procurement: ATCC/DCTD/DTF
        CDNA Library Preparation: Ling Hong/Rubin Laboratory
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
        Plate: LLCM504 row: f column: 17
        High quality sequence start: 38
        High quality sequence stop: 223.
FEATURES             source
    Location/Qualifiers
        1..223
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:3830416"
        /tissue_type="melanotic melanoma"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC_20"
        /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
        EcoRI; cDNA made by oligo-dT priming. Directionally
        cloned into EcoRI/XhoI sites using the following 5'
        adaptor: GGCACGAG(G). Size-selected >500bp for average
        insert size 1.8kb. Library constructed by Ling Hong in
        the laboratory of Gerald M. Rubin (University of
        California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies).
ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  TCCCGGTGCTCTGAGACAT 20
      |||||||
Db   195 TCCCGGTGCTCTGAGACAT 176

RESULT 12
BF026532/c
LOCUS   601672487F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955413 5',
DEFINITION mRNA sequence.
ACCESSION BF026532
VERSION   BF026532.1 GI:10734244
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 225)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-re@mail.nih.gov
        Tissue Procurement: ATCC/DCTD/DTF
        CDNA Library Preparation: Ling Hong/Rubin Laboratory
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
        Plate: LLCM829 row: n column: 22
        High quality sequence start: 40
        High quality sequence stop: 225.
FEATURES             source
    Location/Qualifiers
        1..225
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"

```

```

/clone="IMAGE:3955413"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
Db 197 TCCCGGTTGCTCTGAGACAT 178

RESULT 13
LOCUS BE275637/c
DEFINITION BE275637 227 bp mRNA linear EST 13-JUL-2000
601121162F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988806 5',
mRNA sequence.
ACCESSION BE275637
VERSION BE275637.1 GI:9150595
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW78 row: k column: 15
High quality sequence start: 27
High quality sequence stop: 227.

FEATURES
source Location/Qualifiers
1..227
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2988806"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
Db 199 TCCCGGTTGCTCTGAGACAT 180

RESULT 14
LOCUS BF685843/c
DEFINITION BF685843 230 bp mRNA linear EST 22-DEC-2000
602143136F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304288 5',
mRNA sequence.
ACCESSION BF685843
VERSION BF685843.1 GI:11971251
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1169 row: g column: 09
High quality sequence stop: 230.

FEATURES
source Location/Qualifiers
1..230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4304288"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
Db 182 TCCCGGTTGCTCTGAGACAT 163

RESULT 15
LOCUS BG746689/c
DEFINITION BG746689 232 bp mRNA linear EST 15-MAY-2001
602704010F1 NTH_MGC_15 Homo sapiens cDNA clone IMAGE:4857171 5',
mRNA sequence.
ACCESSION BG746689
VERSION BG746689.1 GI:14057342
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW78 row: k column: 15
High quality sequence start: 27
High quality sequence stop: 227.

FEATURES
source Location/Qualifiers
1..227
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2988806"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 232)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUCM1709 row: d column: 04
High quality sequence stop: 232.

FEATURES
Location/Qualifiers
1..232
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4857171"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TCCCGGTTCCTCTGAGACAT 20
|||||
Db 184 TCCCGGTTCCTCTGAGACAT 165

Search completed: February 5, 2005, 08:11:25
Job time : 2386.67 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 480.738 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-3
Perfect score: 20
Sequence: 1 gccacagtcgcccgtcag 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD235151
2	20	100.0	20	6	BD235165
3	20	100.0	20	6	BD235166
4	20	100.0	60	6	CQ543581
5	20	100.0	127	6	CQ112670
6	20	100.0	127	6	CQ151543
7	20	100.0	127	6	CQ185285
8	20	100.0	127	6	CQ234920
9	20	100.0	127	6	CQ272476
10	20	100.0	127	6	CQ310145
11	20	100.0	127	6	CQ346752
12	20	100.0	387	6	CQ732731
13	20	100.0	513	10	MMU10100
14	20	100.0	513	10	AF136230
15	20	100.0	513	10	AF279286
16	20	100.0	519	4	AF247182
17	20	100.0	537	10	S78284
18	20	100.0	540	6	AX925690
19	20	100.0	541	4	AF245487

C	20	20	100.0	541	4	AF245488	Bos tauru
C	21	20	100.0	541	4	AF245489	Bos tauru
	22	20	100.0	587	6	CQ09589	Sequence
	23	20	100.0	587	6	CQ138575	Sequence
	24	20	100.0	587	6	CQ175406	Sequence
	25	20	100.0	587	6	CQ221990	Sequence
	26	20	100.0	587	6	CQ259935	Sequence
	27	20	100.0	587	6	CQ297711	Sequence
	28	20	100.0	587	6	CQ334058	Sequence
C	29	20	100.0	600	6	AX925692	Sequence
C	30	20	100.0	636	6	BD097037	A BH4 fus
C	31	20	100.0	660	6	AX925694	Sequence
C	32	20	100.0	660	6	AX925696	Sequence
C	33	20	100.0	699	10	MMBCLXL	M.musculus
C	34	20	100.0	702	6	BD084108	X83574
C	35	20	100.0	702	6	BD102202	Method of
C	36	20	100.0	702	9	BT007208	Method fo
C	37	20	100.0	702	10	MMU10101	Homo sapi
C	38	20	100.0	702	12	BT008248	Mus musculus
C	39	20	100.0	726	10	RNU34963	Synthetic
C	40	20	100.0	726	10	S76513	Rattus norv
C	41	20	100.0	737	6	AR054022	U34963
C	42	20	100.0	737	6	AR172595	bcl1-x=apopt
C	43	20	100.0	737	6	IS2012	Sequence
C	44	20	100.0	737	6	AR371662	Sequence 7
C	45	20	100.0	737	6	AR380913	Sequence

ALIGNMENTS

RESULT 1
BD235151
LOCUS BD235151 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xl.
ACCESSION BD235151
VERSION BD235151.1 GI:33044921
KEYWORDS JP 2002519048-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Stein, C.A.
TITLE Oligonucleotide inhibitors of bcl-xl
JOURNAL Patent: JP 2002519048-A 3 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT OS Artificial Sequence
PN JP 2002519048-A/3
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN
PC C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC A61K47/42,
A61K48/00, A61P35/00, C12N15/00
PC A61K47/48 A61K48/00 A61P35/00 C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence',
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
source
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCACAGTCATGCCGTCAG 20
|||||

```
Db          1  GCCACAGTCATGCCCGTCAG 20

RESULT 2
BD235165
LOCUS      20 bp      DNA
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235165
VERSION     BD235165.1 GI:33044935
KEYWORDS   JP 2002519048-A/17.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 17 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/17
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC

C12N15/09,A61K9/127,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PROPYNIL dC
CC PROPYNIL dC
CC PROPYNIL dC
CC PROPYNIL dC
CC PROPYNIL dC
CC PROPYNIL dC
CC PROPYNIL dC
CC PROPYNIL dC
CC PROPYNIL dC
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
FH Key Location/Qualifiers
FT misc_binding (1)..(4)
FT modified_base (2)..(3)
FT modified_base (5)..(5)
FT modified_base (8)..(8)
FT modified_base (9)..(9)
FT modified_base (11)..(11)
FT modified_base (13)..(15)
FT modified_base (17)..(17)
FT modified_base (18)..(18)
FT misc_binding (8)..(9)
FT misc_binding (13)..(15)
FT misc_binding (17)..(20).
FEATURES
    source
    1..20
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
Db 1 GCCACAGTCATGCCCGTCAG 20

RESULT 4
CQ543581/c
LOCUS      60 bp      DNA
DEFINITION Sequence 13216 from Patent WO0210449.
ACCESSION  CQ543581
VERSION     CQ543581.1 GI:41509845
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE      Oligonucleotide library for detecting rna transcripts and splice
           variants that populate a transcriptome
JOURNAL    Patent: WO 0210449-A 13216 07-FEB-2002;
           Compugen Inc. (US)
FEATURES
    source
    1..60
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 60;

Db          1  GCCACAGTCATGCCCGTCAG 20

RESULT 3
BD235166
LOCUS      20 bp      DNA
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235166
VERSION     BD235166.1 GI:33044936
KEYWORDS   JP 2002519048-A/18.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 18 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/18
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
```

Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 36 GCCACAGTCATGCCCGTCAG 17

RESULT 5
LOCUS CQ112670 127 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 21529 from Patent WO0157272.
ACCESSION CQ112670
VERSION CQ112670.1 GI:41082540
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 21529 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 6
LOCUS CQ151543 127 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 21565 from Patent WO0157276.
ACCESSION CQ151543
VERSION CQ151543.1 GI:41158893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 21565 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 5.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 7
LOCUS CQ185285 127 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 16681 from Patent WO0157274.
ACCESSION CQ185285
VERSION CQ185285.1 GI:41180300
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 16681 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
1.6-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 8
LOCUS CQ234920 127 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 21759 from Patent WO0157273.
ACCESSION CQ234920
VERSION CQ234920.1 GI:41218197
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 21759 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..127
/organism="Homo sapiens"

```
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
= 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"

ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 9
LOCUS      CQ272476      127 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 20737 from Patent WO0157277.
ACCESSION  CQ272476
VERSION     CQ272476.1 GI:41245080
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human fetal liver
JOURNAL     Patent: WO 0157277-A 20737 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..127
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
            = 4.1-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
            HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
            1.00e-65"

ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 10
LOCUS      CQ310145      127 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21250 from Patent WO0186003.
ACCESSION  CQ310145
VERSION     CQ310145.1 GI:41270722
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human lung
JOURNAL     Patent: WO 0186003-A 21250 15-NOV-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..127
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
            2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
            AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
            1.00e-65"

ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 11
LOCUS      CQ346752      127 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 20846 from Patent WO0157275.
ACCESSION  CQ346752
VERSION     CQ346752.1 GI:41295823
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human brain
JOURNAL     Patent: WO 0157275-A 20846 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..127
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
            2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
            AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
            1.00e-65"

ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 12
LOCUS      CQ732731      387 bp      DNA      linear      PAT 03-FEB-2004
DEFINITION Sequence 18665 from Patent WO02068579.
ACCESSION  CQ732731
VERSION     CQ732731.1 GI:42313858
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE       Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
JOURNAL     Patent: WO 02068579-A 18665 06-SEP-2002;
            PE Corporation (US)
```



```

FEATURES
  source
    Location/Qualifiers
      1..387
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

ORIGIN
  Query Match      100.0%; Score 20; DB 6; Length 387;
  Best Local Similarity 100.0%; Pred. No. 30;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 347 GCCACAGTCATGCCCGTCAG 328

RESULT 13
MMU10100/c
LOCUS
DEFINITION Mus musculus bcl-x short (bcl-x long) mRNA, complete cds.
ACCESSION U10100
VERSION U10100.1 GI:506645
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 513)
  Fang, W., Rivard, J.J., Mueller, D.L. and Behrens, T.W.
  Cloning and molecular characterization of mouse bcl-x in B and T
  lymphocytes
  JOURNAL J. Immunol. 153 (10), 4388-4398 (1994)
  MEDLINE 95052604
  PUBMED 7963517
  REFERENCE 2 (bases 1 to 513)
  Behrens, T.W.
  Direct Submission
  TITLE Submitted (26-MAY-1994) Timothy W. Behrens, Medicine, University of
  Minnesota, 515 Delaware St. S.E., Minneapolis, MN 55455, USA
  JOURNAL
  FEATURES
    source
      1..513
      /organism="Mus musculus"
      /mol_type="mRNA"
      /db_xref="taxon:10090"
      /cell_lines="WEHI 265.1 RNA"
      /note="alternatively spliced transcript of bcl-x long,
      GenBank Accession Number U10101"
      1..513
      /gene="bcl-x long"
      1..513
      /gene="bcl-x long"
      /codon_start=1
      /product="bcl-x short"
      /protein_id="AA82172.1"
      /db_xref="GI:506646"
      /translation="MSQSNRELVVDFLSYKLSQKYSQSFSDVEENRTEAPEETEPE
      RETPSAINGNPSWHLADSPVNGATGHSLSLDAREVTPMAAVKQALREAGDEPELRVR
      RAPSDLTSLQHIPTGTAYQSFQDTPFDLYGNNAAESRKQERFNRWFLTGMTVAGV
      VLLGSLFSRK"

gene
  CDS
    Query Match      100.0%; Score 20; DB 10; Length 513;
    Best Local Similarity 100.0%; Pred. No. 29;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

RESULT 14
AF136230/c
LOCUS
DEFINITION Rattus norvegicus bcl-x short mRNA, complete cds.
ACCESSION AF136230
VERSION AF136230.1 GI:4928687
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.
  1 (bases 1 to 513)
  He, X.J., Jin, K.L., Graham, S.H. and Simon, R.P.
  Direct Submission
  TITLE Submitted (22-MAR-1999) Neurology, University of Pittsburgh, 3500
  Terrace Street, Pittsburgh, PA 15213, USA
  JOURNAL
  FEATURES
    source
      1..513
      /organism="Rattus norvegicus"
      /mol_type="mRNA"
      /strain="Sprague-Dawley"
      /db_xref="taxon:10116"
      /tissue_type="brain"
      /note="Isolated from an ischemic brain"
      1..513
      /codon_start=1
      /product="bcl-x short"
      /protein_id="AAD33683.1"
      /db_xref="GI:4928688"
      /translation="MSQSNRELVVDFLSYKLSQKYSQSFSDVEENRTEAPEETEPE
      RETPSAINGNPSWHLADSPVNGATGHSLSLDAREVTPMAAVKQALREAGDEPELRVR
      RAPSDLTSLQHIPTGTAYQSFQDTPFDLYGNNAAESRKQERFNRWFLTGMTVAGV
      VLLGSLFSRK"

ORIGIN
  Query Match      100.0%; Score 20; DB 10; Length 513;
  Best Local Similarity 100.0%; Pred. No. 29;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

RESULT 15
AF279286/c
LOCUS
DEFINITION Rattus norvegicus bcl-x short form mRNA, complete cds.
ACCESSION AF279286
VERSION AF279286.1 GI:8896160
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.
  1 (bases 1 to 513)
  Cao, G., Chen, J. and Chen, D.
  Bcl-Xs expression and its role in brain ischemia
  Unpublished
  JOURNAL
  REFERENCE 2 (bases 1 to 513)
  Cao, G., Chen, J. and Chen, D.
  Direct Submission
  TITLE Submitted (16-JUN-2000) Neurology, University of Pittsburgh, 3500
  Terrace Street, Pittsburgh, PA 15261, USA
  JOURNAL
  FEATURES
    source
      1..513
      /organism="Rattus norvegicus"
      /mol_type="mRNA"
      /strain="Sprague-Dawley"
      /db_xref="taxon:10116"
      /tissue_type="cerebellum"
      /dev_stage="postnatal 1 week"
      1..513
      /codon_start=1

```

```
/product="bel-x short form"  
/protein_id="AAP81262.1"  
/db_xref="GI:8896161"  
/translation="MSQSNRELVVDFLSYKLSQKGYWSQFSDVVENRTEAPEETEPE  
RTPPSAINGNPGWHLADSPAVRGATGHSSLDAREVIPMAAVKQALREAGDEFELRYR  
RAFSDLTSLQHLITPGTAYQSFQDTFVDLYGNNAASERKQGERFNRWFLTGMTVAGV  
VLLGSLFSRK"
```

ORIGIN

```
Query Match      100.0%; Score 20; DB 10; Length 513;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY      1 GCCACAGTCATGCCCGTCAG 20  
         |||||||  
Db      473 GCCACAGTCATGCCCGTCAG 454
```

Search completed: February 4, 2005, 23:30:38
Job time : 482.738 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169a-3

Perfect score: 20

Sequence: 1 gccacagtcagcccgctcag 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	Az46973 Bcl-Xl MR
C 2	20	100.0	25	12	Adp14975 Renal cel
C 3	20	100.0	25	12	Adp17304 Renal cel
C 4	20	100.0	60	6	Abn40468 Human spl
5	20	100.0	127	4	Aba72432 Human foe
6	20	100.0	127	4	Aa152843 Probe #21
7	20	100.0	127	4	Aba38215 Probe #16
8	20	100.0	127	4	Aak47008 Human bon
9	20	100.0	127	4	Aak20855 Human bra
10	20	100.0	127	4	Abse46769 Human liv
11	20	100.0	127	6	Abse21259 Human gen
C 12	20	100.0	179	12	Ach84269 Human gen
C 13	20	100.0	299	10	AcD94503 Human col
C 14	20	100.0	337	10	Adk66037 Standard
C 15	20	100.0	492	9	Ach46093 Human inf
C 16	20	100.0	540	12	Adh52634 Chinese h
C 17	20	100.0	587	4	Abse59891 Human foe
18	20	100.0	587	4	Aa139762 Probe #84
19	20	100.0	587	4	Abse28336 Probe #68
20	20	100.0	587	4	Aak34040 Human bon
21	20	100.0	587	4	Aak08161 Human bra

22	20	100.0	587	4	Abse33839 Human liv
23	20	100.0	587	6	Abse08825 Human gen
C 24	20	100.0	587	12	Ach70569 Human gen
C 25	20	100.0	600	12	Adh52636 Chinese h
C 26	20	100.0	636	4	Aah48169 Mutant bc
C 27	20	100.0	660	12	Adh52638 Chinese h
C 28	20	100.0	660	12	Adh52640 Chinese h
C 29	20	100.0	702	5	Aah43464 cDNA clon
C 30	20	100.0	702	12	Adm45994 Human apo
C 31	20	100.0	737	2	Aaq81699 Human thy
C 32	20	100.0	737	10	Abz83507 Toxicolog
C 33	20	100.0	737	11	Adi32132 Human cdn
C 34	20	100.0	863	12	Adh52632 Chinese h
C 35	20	100.0	926	2	Aaq81698 Human thy
C 36	20	100.0	926	2	AAT40079 Bcl-XL ge
C 37	20	100.0	926	3	Aaz93614 Bcl-x gen
C 38	20	100.0	926	4	Aas15189 Human bcl
C 39	20	100.0	926	4	AAC90810 Human bcl
C 40	20	100.0	926	6	Abk84766 Human cdn
C 41	20	100.0	926	8	Abt16641 Human bcl
C 42	20	100.0	926	10	Add56779 Human bcl
C 43	20	100.0	926	10	Aad64187 Human bcl
C 44	20	100.0	926	11	Adi32104 Human cdn
C 45	20	100.0	926	12	Adh52630 Human ant

ALIGNMENTS

RESULT 1
AAZ46973
ID AAZ46973 standard; DNA; 20 BP.
XX AC
AC AAZ46973;
XX AC
DT 14-APR-2000 (first entry)
XX Bcl-Xl mRNA specific antisense oligo C.
DE Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.
XX Homo sapiens.
OS WO200001393-A2.
XX PF
XX 02-JUL-1999; 99WO-US015250.
XX PD 13-JAN-2000.
XX PR
XX 02-JUL-1998; 98US-00109614.
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX Stein CA;
XX WPI; 2000-137140/12.
XX PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.
XX PS Claim 1; Fig 1; 69pp; English.
XX CC The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra
CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
CC represent antisense oligos specific for the bcl-Xl mRNA
XX
SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 1 GCCACAGTCATGCCCGTCAG 20

RESULT 2
ADP14975/c
ID ADP14975 standard; DNA; 25 BP.
XX
AC ADP14975;
XX
DT 26-AUG-2004 (first entry)
XX
DE Renal cell carcinoma differentially expressed gene probe #1380.
XX
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
OS Homo sapiens.
XX
PN WO2004048933-A2.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-US037481.
XX
PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
XX WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 1711; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of

CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX

SQ Sequence 25 BP; 3 A; 7 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 23 GCCACAGTCATGCCCGTCAG 4

RESULT 3
ADP17304/c
ID ADP17304 standard; DNA; 25 BP.
XX
AC ADP17304;
XX
DT 26-AUG-2004 (first entry)
XX
DE Renal cell carcinoma differentially expressed gene probe #3709.
XX
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
OS Homo sapiens.
XX
PN WO2004048933-A2.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-US037481.
XX
PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
XX WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 4040; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to

CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX

SQ Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 22 GCCACAGTCATGCCCGTCAG 3

RESULT 4

ABN40468/c
ID ABN40468 standard; DNA; 60 BP.

XX

AC ABN40468;

XX

DT 15-JUL-2002 (first entry)

XX

DE Human spliced transcript detection oligonucleotide SEQ ID NO:13216.

XX

KW Human; mouse; rat; splice transcript; detection; RNA transcript;

XX

KW splice variant; transcriptome; oligonucleotide library; ss.

XX

OS Homo sapiens.

XX

PN WO200210449-A2.

XX

PD 07-FEB-2002.

XX

PF 20-JUL-2001; 2001WO-IB001903.

XX

PR 28-JUL-2000; 2000US-0221607P.

XX

PR 02-MAY-2001; 2001US-0287724P.

XX

PA (COMP-) COMPUGEN INC.

XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX

WPI; 2002-257383/30.

XX

PT New oligonucleotide libraries comprising oligonucleotides which
selectively hybridize to mRNAs transcribed from a transcription unit of a
genome, useful for detecting tissue-, pathology-, and developmental-

PT specific genes.

XX

PS Example 1; SEQ ID NO 13216; 47pp; English.

XX

CC The present invention describes oligonucleotide libraries for detecting
messenger RNAs that populate a (sub-)transcriptome, where the (sub-
)transcriptome comprises messenger RNAs transcribed from multiple
transcription units that populate a genome. The library comprises several
oligonucleotides, each capable of hybridizing selectively to a set of
messenger RNAs transcribed from a given transcription unit of the genome,
which encodes one or more messenger RNA splice variants. The

CC oligonucleotide libraries are useful for detecting mRNAs from a
biological sample, in expression profiling studies, in qualitatively or
quantitatively characterizing the corresponding transcriptome, and in
detecting RNA transcripts and splice variants of human or animal
transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a particular
biological or pathological state, and so allowing the detection of tissue
- and pathology-specific genes such as those genes only expressed in
specific tissue under a specific pathological condition; to detect
developmental specific genes; and to detect RNA transcripts and splice
variants of a transcriptome of a patient suffering from a particular
disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
rats, humans and mice, which are used in the exemplification of the
present invention. N.B. The sequence data for this patent did not form
part of the printed specification, but was obtained in electronic format

CC

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 6 A; 18 C; 20 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 36 GCCACAGTCATGCCCGTCAG 17

RESULT 5

ABA72432
ID ABA72432 standard; DNA; 127 BP.

XX

AC ABA72432;

XX

DT 01-FEB-2002 (first entry)

XX

DE Human foetal liver single exon nucleic acid probe #20737.

XX

KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX

OS Homo sapiens.

XX

PN WO200157277-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US000669.

XX

PR 04-FEB-2000; 2000US-0180312P.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 30-JUN-2000; 2000US-00608408.

XX

PR 03-AUG-2000; 2000US-00632366.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

WPI; 2001-483447/52.

XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human foetal liver.
XX

PS Claim 4; SEQ ID NO 20737; 639pp + Sequence Listing; English.

XX

CC The invention relates to a single exon nucleic acid probe for measuring
human gene expression in a sample derived from human foetal liver. The
single exon nucleic acid probes may be used for predicting, measuring and
displaying gene expression in samples derived from human foetal liver. The
present sequence is a single exon nucleic acid probe of the invention.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 6

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention

Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.7; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 30 GCCACAGTCATGCCCGTCAG 49
|||||

RESULT 10
ABS46769
ID ABS46769 standard; DNA; 127 BP.
XX AC ABS46769;
XX DT
XX DE 25-FEB-2003 (first entry)
XX Human liver single exon probe, SEQ ID NO 21759.
XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX OS Homo sapiens.
XX FN WO200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000664.
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX Claim 4; SEQ ID NO 21759; 658pp; English.
XX The invention relates to a single exon nucleic acid probe (SEN) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match      100.0%; Score 20; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 11
ABS21259
ID ABS21259 standard; DNA; 127 BP.
AC
XX ABS21259;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 21250.
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 4; SEQ ID NO 21250; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
```


PF Z1-SEP-1999; 9905-00406117.

XX DE standardized polynucleotide system polynucleotide #8.

XX DE standardized polynucleotide system polynucleotide #8.

KW ss; standardized polynucleotide system; medical diagnosis;
KW functional genomics; sample analysis; pharmacogenomics; sample analysis.
OS Unidentified.
XX
PN DE10209071-A1.
XX
XX 25-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01009071.
PF
XX 28-FEB-2002; 2002DE-01009071.
PR
XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
XX
XX Koehler T, Rost A;
PI
XX WPI; 2003-732912/70.
XX
XX Standardized polynucleotide system, useful for quantitative, real-time
PT determination of nucleic acid, comprises stabilized standards, primers
PT and probe.
XX
XX Claim 1; Page 7; 38pp; German.
PS
XX The present invention relates to a standardized polynucleotide system,
CC which comprises at least one carrier nucleic acid, at least 3
CC oligonucleotides, as primers and target-specific, fluorescently labeled
CC probe and optionally at least one set of stabilized controls (standard
CC RNA or DNA) of known concentration and instructions. The system comprises
CC any of 20 sets of one control, two primers and one target-specific probe.
CC The standardized polynucleotide system can be used for quantitative, real
CC -time detection of target nucleic acids, especially analysis of genes or
CC gene products, e.g. for individualized medical diagnosis, in veterinary
CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,
CC pharmaceutical testing, analysis of food or environmental samples and
CC also for ultra-sensitive detection of proteins by immuno-PCR. The present
CC sequence is a polynucleotide used in the system of the invention.
XX
XX Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 10; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCACAGTCATGCCCGTCAG 20
Db 259 GCCACAGTCATGCCCGTCAG 240
RESULT 15
ACH46093/C
ID ACH46093 standard; cDNA; 492 BP.
XX
AC ACH46093;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human infant brain cDNA #156.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
PF
XX 30-JUL-2001; 2001US-00918995.
PR
XX

PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
DR
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 33305; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations,
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 9; Length 492;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCACAGTCATGCCCGTCAG 20
Db 443 GCCACAGTCATGCCCGTCAG 424
Search completed: February 4, 2005, 21:52:40
Job time : 261.033 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-3
Perfect score: 20
Sequence: 1 gccacagtcagcccgtag 20
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	119	2	BF840557 MR1-HT106
C 2	20	100.0	133	2	AW606507 MR2-HT038
C 3	20	100.0	140	2	BF948716 CM2-NN115
C 4	20	100.0	167	2	BF929309 IL2-NT020
C 5	20	100.0	177	9	CG642691 OST379295
C 6	20	100.0	194	2	BF880488 QV3-ET017
C 7	20	100.0	216	2	BF806802 PM2-CI011
C 8	20	100.0	227	9	CG656719 OST429779
C 9	20	100.0	233	1	AI904167 CM-BT043
C 10	20	100.0	253	9	CG659215 OST436826
C 11	20	100.0	254	7	T28063 EST26052 Hu
C 12	20	100.0	283	2	BF823588 RCS-RT005
C 13	20	100.0	332	2	AW820481 QV2-ST029
C 14	20	100.0	337	9	CG667740 OST461931
C 15	20	100.0	338	9	CG581705 OST222203
C 16	20	100.0	339	2	BE925384 PM0-AN008
C 17	20	100.0	356	2	AW244806 BR_END13C
C 18	20	100.0	374	9	CG524482 OST98550
C 19	20	100.0	374	9	CG631933 OST349236
C 20	20	100.0	391	9	CG624538 OST328585
C 21	20	100.0	396	4	BM818649 K-EST0085
C 22	20	100.0	403	9	CG632613 OST351228
C 23	20	100.0	412	9	CG559660 OST178957
C 24	20	100.0	413	9	CG663330 OST448394

RESULT 1

BF840557/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

C 25 20 100.0 415 9 CG531843
C 26 20 100.0 418 4 BI051278
C 27 20 100.0 418 4 BM741875
C 28 20 100.0 428 9 CG638384
C 29 20 100.0 442 1 AA903741
C 30 20 100.0 447 4 BM818387
C 31 20 100.0 466 9 CG592069
C 32 20 100.0 472 1 AI180733
C 33 20 100.0 475 5 BQ331598
C 34 20 100.0 482 2 BE378810
C 35 20 100.0 484 9 CG604974
C 36 20 100.0 486 9 CG598768
C 37 20 100.0 495 1 AA823283
C 38 20 100.0 496 7 CF725764
C 39 20 100.0 499 9 CG615667
C 40 20 100.0 501 4 BM090012
C 41 20 100.0 504 9 CG607848
C 42 20 100.0 508 9 CG607263
C 43 20 100.0 512 9 CG642256
C 44 20 100.0 512 9 CG646113
C 45 20 100.0 514 9 CG625069

ALIGNMENTS

BF840557 119 bp mRNA linear EST 13-JAN-2001
MR1-HT1067-011200-001-a10 HT1067 Homo sapiens cdNA, mRNA sequence.
BF840557
BF840557.1 GI:12193055
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 119)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MRI&t2=MRI-HT1067-
011200-001-a10&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 48
High quality sequence stop: 119.
Location/Qualifiers
1. 119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT1067"
/notes="Organ: head neck; Vector: puc18; Site:1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 91 GCCACAGTCATGCCCGTCAG 72

RESULT 2

AW606507
LOCUS MR2-HT0380-010200-101-f06 HT0380 Homo sapiens cDNA, mRNA sequence. EST 23-MAR-2000
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133)
HCGP <http://www.ludwig.org.br/ORESTES>.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-HT0380-010200-101-f06&t3=2000-02-01&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 133.
Location/Qualifiers
1. .133
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0380"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 140)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bais,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 140.
Location/Qualifiers
1. .140
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1152"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match 100.0%; Score 20; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 83 GCCACAGTCATGCCCGTCAG 102

RESULT 4

BF929309

LOCUS IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 140.
Location/Qualifiers
1. .140
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1152"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match 100.0%; Score 20; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 83 GCCACAGTCATGCCCGTCAG 102

RESULT 4

BF929309

LOCUS IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 140.
Location/Qualifiers
1. .140
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1152"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match 100.0%; Score 20; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 83 GCCACAGTCATGCCCGTCAG 102

RESULT 4

BF929309

LOCUS IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 140.
Location/Qualifiers
1. .140
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1152"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match 100.0%; Score 20; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 83 GCCACAGTCATGCCCGTCAG 102

RESULT 4

BF929309

LOCUS IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 140.
Location/Qualifiers
1. .140
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1152"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match 100.0%; Score 20; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 83 GCCACAGTCATGCCCGTCAG 102

RESULT 4

BF929309

LOCUS IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 140.
Location/Qualifiers
1. .140
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1152"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match 100.0%; Score 20; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 83 GCCACAGTCATGCCCGTCAG 102

RESULT 4

BF929309

LOCUS IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 140.
Location/Qualifiers
1. .140
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1152"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 167.

Location/Qualifiers

1. .167

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="NT0202"

/note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 167;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20

|||||

66 GCCACAGTCATGCCCGTCAG 85

RESULT 5

CG642691/c

LOCUS

DEFINITION CG642691 177 bp DNA linear GSS 02-OCT-2003

OST379295 Mus musculus 129Sv/Ev Mus musculus genomic clone

OST379295, genomic survey sequence.

ACCESSION CG642691

CG642691.1 GI:37466540

VERSION GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 177)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P.P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

TITLE

JOURNAL

COMMENT

OmiBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .177.

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST379295"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

RESULT 6

BF880488

LOCUS

DEFINITION BF880488 194 bp mRNA linear EST 17-JAN-2001

QV3-ET0175-011200-514-a04 ET0175 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF880488

VERSION BF880488.1 GI:12270718

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 194)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

PURMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0175-011200-514-a04&t3=2000-12-01&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 17

High quality sequence stop: 194.

Location/Qualifiers

1. .194

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="ET0175"

/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;

FEATURES

source

Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 125 GCCACAGTCATGCCCGTCAG 144

RESULT 7

BF806802 216 bp mRNA linear EST 12-JAN-2001
LOCUS PM2-CI0111-091100-004-b10 CI0111 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF806802
ACCESSION BF806802.1 GI:12135791
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 216)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,F.S., Bucher,P., Jorgeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800

TITLE

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-091100-004-b10&t3=2000-11-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 216.

FEATURES

source
1..216
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CI0111"
/note="Organ: colon ins; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 50;

Matches

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 65 GCCACAGTCATGCCCGTCAG 84

RESULT 8

CG56719/c 227 bp DNA linear GSS 02-OCT-2003
LOCUS OST429779 Mus musculus 129Sv/Ev Mus musculus genomic clone
DEFINITION OST429779, genomic survey sequence.
ACCESSION CG56719
VERSION CG56719.1 GI:37480568
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 227)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.
Location/Qualifiers
1..227
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST429779"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

TITLE

JOURNAL

COMMENT

FEATURES

source
1..227
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST429779"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
|||||
Db 87 GCCACAGTCATGCCCGTCAG 68

RESULT 9

AI904167/c 233 bp mRNA linear EST 30-MAR-2000
LOCUS CM-BT043-090299-089 BT043 Homo sapiens cDNA, mRNA sequence.
DEFINITION AI904167
ACCESSION AI904167.1 GI:6494554
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 233)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/seg/gethtml.pl?tl=CM&t2=CM-BT043-089.html>) &t3=090299&t4=1)

Seq primer: puc 18 forward.

Location/Qualifiers

1. .233
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/dev stage="Adult"
/clone_lib="BT043"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20

Db 96 GCCACAGTCATGCCCGTCAG 77

RESULT 10

CG659215/c

LOCUS

CG659215 253 bp DNA linear GSS 02-OCT-2003

OST436826 Mus musculus 129Sv/Ev Mus musculus genomic clone

OST436826, genomic survey sequence.

ACCESSION

CG659215

VERSION

CG659215.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 253)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,

Piggott,J., BeltrandeRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,

Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,

Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,

Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,

Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,

Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

FEATURES

source

1. .253
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST436826"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 253;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20

Db 67 GCCACAGTCATGCCCGTCAG 48

RESULT 11

T28063/c

LOCUS

T28063 254 bp mRNA linear EST 06-SEP-1995

DEFINITION

EST26052 Human Brain Homo sapiens cDNA 5' end similar to bcl-x

(BT:3191), mRNA sequence.

VERSION

T28063.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 254)

Adams,M.D., Kervlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

Bult,C.J., Lee,N., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D.,

White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,

Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,

Fitzgerald,D.M., Fitchugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,

Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S.,

Kellie,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,

Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,

Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,

Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,

Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,

Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,

Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,

Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,

Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,

Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,

Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns

Based Upon 83 Million Basepairs of cDNA Sequence

Nature 377, 3-174 (1995)

96026280

7566098

Other ESTs: THC20696

Contact: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database

(tdbinfo@tdb.tigr.org)

Seq primer: M13 Reverse.

Location/Qualifiers

1. .254

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):101016"
/db_xref="taxon:9606"
/clone_lib="Human Brain"
/note="Organ: brain"

ORIGIN
Query Match      100.0%; Score 20; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 194 GCCACAGTCATGCCCGTCAG 175

RESULT 12
BF823588      283 bp mRNA linear EST 13-JAN-2001
LOCUS RC5-RT0055-221200-011-G02 RT0055 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF823588
ACCESSION BF823588
VERSION BF823588.1 GI:12164528
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 283)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC5&t2=RC5-RT0055-
221200-011-G02&t3=2000-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 283.
FEATURES
source
1..283
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="RT0055"
/note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 263 GCCACAGTCATGCCCGTCAG 244

RESULT 14
CG667740      337 bp DNA linear GSS 02-OCT-2003
LOCUS OST461931 Mus musculus 129sv/Ev Mus musculus genomic clone
DEFINITION OST461931, genomic survey sequence.

```

```

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 111 GCCACAGTCATGCCCGTCAG 130

RESULT 13
AW820481      332 bp mRNA linear EST 17-MAY-2000
LOCUS QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW820481
ACCESSION AW820481
VERSION AW820481.1 GI:7913475
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 332)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=QV2-ST0298-140
200-042-f12&t3=2000-02-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
FEATURES
source
1..332
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ST0298"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 263 GCCACAGTCATGCCCGTCAG 244

RESULT 14
CG667740      337 bp DNA linear GSS 02-OCT-2003
LOCUS OST461931 Mus musculus 129sv/Ev Mus musculus genomic clone
DEFINITION OST461931, genomic survey sequence.

```



```

ACCESSION      CG667740
VERSION        CG667740.1  GI:37491589
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 337)
               Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
               Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
               Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
               Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
               Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
               Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
               Zhu, Q., Person, C. and Sands, A.T.
               Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
               screen to identify potential targets for therapeutic intervention
               Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
               Contact: Zambrowicz BP
               OmniBank
               Lexicon Genetics Incorporated
               4000 Research Forest Drive, The Woodlands, TX 77381, USA
               Email: materials@lexgen.com
               Gene trap sequence tag generated by 3' RACE from mouse ES cells as
               described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
               Class: Gene Trap.
               Location/Qualifiers
               1..337
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="129Sv/Ev"
               /db_xref="taxon:10090"
               /clones="OST461931"
               /cell_type="embryonic stem cell"
               /clone_lib="Mus musculus 129Sv/Ev"

TITLE
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA

FEATURES
source
1..337
Location/Qualifiers
1..338
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="129Sv/Ev"
/db_xref="taxon:10090"
/call_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 338;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 105 GCCACAGTCATGCCCGTCAG 86
   |||||

Search completed: February 5, 2005, 08:11:31
Job time : 2390.67 secs

RESULT 15
CG581705/c
LOCUS
DEFINITION   CG581705 338 bp DNA linear GSS 02-OCT-2003
               OST222203 Mus musculus 129Sv/Ev Mus musculus genomic clone
               OST222203, genomic survey sequence.
VERSION      CG581705
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 338)
               Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
               Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
               Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
               Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
               Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
               Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
               Zhu, Q., Person, C. and Sands, A.T.
               Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
               screen to identify potential targets for therapeutic intervention
               Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
               Contact: Zambrowicz BP
               OmniBank
               Lexicon Genetics Incorporated
               4000 Research Forest Drive, The Woodlands, TX 77381, USA

```

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 480.738 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-4
Perfect score: 20
Sequence: 1 ctgcgatccgactccaacat 20
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD235152
2	20	100.0	20	6	BD235167
3	20	100.0	555	6	CQ113695
4	20	100.0	555	6	CQ152574
5	20	100.0	555	6	CQ185831
6	20	100.0	555	6	CQ235904
7	20	100.0	555	6	CQ273477
8	20	100.0	555	6	CQ310858
9	20	100.0	555	6	CQ347773
10	20	100.0	600	6	CQ100639
11	20	100.0	600	6	CQ139631
12	20	100.0	600	6	CQ175964
13	20	100.0	600	6	CQ222999
14	20	100.0	600	6	CQ260961
15	20	100.0	600	6	CQ298444
16	20	100.0	600	6	CQ335104
17	20	100.0	636	6	BD097037
18	20	100.0	702	6	BD084108
19	20	100.0	702	6	BD102202

C 20	20	100.0	702	9	BT007208
C 21	20	100.0	702	12	BT008248
C 22	20	100.0	723	9	HSU72398
C 23	20	100.0	747	6	AX127722
C 24	20	100.0	926	6	AR054021
C 25	20	100.0	926	6	AR118504
C 26	20	100.0	926	6	AR124952
C 27	20	100.0	926	6	AR144311
C 28	20	100.0	926	6	AR172594
C 29	20	100.0	926	6	BD243042
C 30	20	100.0	926	6	CQ765842
C 31	20	100.0	926	6	E58777
C 32	20	100.0	926	6	I52011
C 33	20	100.0	926	6	AR371661
C 34	20	100.0	926	6	AR380885
C 35	20	100.0	926	6	AX839772
C 36	20	100.0	926	6	AX925686
C 37	20	100.0	926	9	HSBCLXL
C 38	20	100.0	1163	4	AB080951
C 39	20	100.0	1236	6	AX085490
C 40	20	100.0	1252	4	AB073983
C 41	20	100.0	1455	6	AX085496
C 42	20	100.0	2575	6	CQ827863
C 43	20	100.0	2575	9	EC019307
C 44	20	100.0	7372	6	E23357
C 45	20	100.0	81171	2	AC016218

ALIGNMENTS

RESULT 1
LOCUS BD235152 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xl.
ACCESSION BD235152
VERSION BD235152.1 GI:33044922
KEYWORDS JP 2002519048-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Stein,C.A.
TITLE Oligonucleotide inhibitors of bcl-xl
JOURNAL Patent: JP 2002519048-A 4 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

COMMENT
OS Artificial Sequence
PN JP 2002519048-A/4
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PI 02-JUL-1998 US 09/109614
CY A STEIN

PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCGATCCGACTCCAACAT 20
|||||||

```

Db      1 CTGCGATCCGACTCACCACAT 20
RESULT 2
BD235167
LOCUS      BD235167
DEFINITION Oligonucleotide inhibitors of bcl-xL
ACCESSION BD235167
VERSION    BD235167.1 GI:33044937
KEYWORDS   JP 2002519048-A/19
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 19 02-JUL-2002;
            THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
            PN JP 2002519048-A/19
            PD 02-JUL-2002
            PF 02-JUL-1999 JP 2000557839
            PR 02-JUL-1998 US 09/109614
            PI CY A STEIN
            PC
            C12N15/09,A61K9/127,A61K31/711,A61K31/712,A61K31/7125, PC
            A61K47/42,
            PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
            CC ANTISENSE OLIGONUCLEOTIDE
            CC PHOSPHOROTHIOATE LINKAGE
            CC PHOSPHOROTHIOATE LINKAGE
            CC PHOSPHOROTHIOATE LINKAGE
            CC PHOSPHOROTHIOATE LINKAGE
            CC PHOSPHOROTHIOATE LINKAGE
            CC PROPENYL dc
            CC PROPENYL dt
            CC PROPENYL dc
            CC PROPENYL dt
            CC PROPENYL dc
            CC PROPENYL dt
            CC PROPENYL dc
            FH Key
            FT misc_binding (2)..(3)
            FT misc_binding (7)..(9)
            FT misc_binding (12)..(14)
            FT misc_binding (16)..(20)
            FT modified_base (1)..(1)
            FT modified_base (2)..(2)
            FT modified_base (4)..(4)
            FT modified_base (7)..(7)
            FT modified_base (8)..(9)
            FT modified_base (12)..(12)
            FT modified_base (13)..(13)
            FT modified_base (16)..(17)
FEATURES   source
            Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGCGATCCGACTCACCACAT 20
        |||||
Db      1 CTGCGATCCGACTCACCACAT 20
RESULT 3
CQ113695
LOCUS      CQ113695
DEFINITION Sequence 22554 from Patent WO0157272.
ACCESSION CQ113695
VERSION    CQ113695.1 GI:41083565
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human placenta
JOURNAL    Patent: WO 0157272-A 22554 09-AUG-2001;
            Aemica, Inc. (US)
FEATURES   Location/Qualifiers
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
            0.99-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST_HUMAN
            HIT: BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGCGATCCGACTCACCACAT 20
        |||||
Db      63 CTGCGATCCGACTCACCACAT 82
RESULT 4
CQ152574
LOCUS      CQ152574
DEFINITION Sequence 22596 from Patent WO0157276.
ACCESSION CQ152574
VERSION    CQ152574.1 GI:41159924
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human bone marrow
JOURNAL    Patent: WO 0157276-A 22596 09-AUG-2001;
            Aemica, Inc. (US)
FEATURES   Location/Qualifiers
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
            = 4.7-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST_HUMAN
            HIT: BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGCGATCCGACTCACCACAT 20
        |||||
Db      63 CTGCGATCCGACTCACCACAT 82
RESULT 5
CQ185831
LOCUS      CQ185831
DEFINITION Sequence 22554 from Patent WO0157272.
ACCESSION CQ113695
VERSION    CQ113695.1 GI:41083565
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human placenta
JOURNAL    Patent: WO 0157272-A 22554 09-AUG-2001;
            Aemica, Inc. (US)
FEATURES   Location/Qualifiers
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
            0.99-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST_HUMAN
            HIT: BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGCGATCCGACTCACCACAT 20
        |||||
Db      63 CTGCGATCCGACTCACCACAT 82

```

```

LOCUS       CQ185831               555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION  Sequence 17227 from Patent WO0157274.
ACCESSION   CQ185831
VERSION     CQ185831.1 GI:41180846
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human heart
JOURNAL     Patent: WO 0157274-A 17227 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
            1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
            BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACCACAT 20
    |||||
Db 63 CTGCGATCCGACTCACCACAT 82

RESULT 6
LOCUS       CQ235904               555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION  Sequence 22743 from Patent WO0157273.
ACCESSION   CQ235904
VERSION     CQ235904.1 GI:41219182
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
            ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
            3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
            60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
            August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
            (03.10.00)<150> US 60/236,359<151> 27 September 2000
            (27.09.00)<150> US 60/234,687<151> 21 September 2000
            (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
            Molecular Dynamics Sequence Listing Engine
            Patent: WO 0157273-A 22743 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
            = 1.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
            HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS       CQ185831               555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION  Sequence 17227 from Patent WO0157274.
ACCESSION   CQ185831
VERSION     CQ185831.1 GI:41180846
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human heart
JOURNAL     Patent: WO 0157274-A 17227 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN PETAL LIVER, SIGNAL
            = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
            HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACCACAT 20
    |||||
Db 63 CTGCGATCCGACTCACCACAT 82

RESULT 7
LOCUS       CQ273477               555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION  Sequence 21738 from Patent WO0157277.
ACCESSION   CQ273477
VERSION     CQ273477.1 GI:41246081
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human fetal liver
JOURNAL     Patent: WO 0157277-A 21738 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN PETAL LIVER, SIGNAL
            = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
            HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACCACAT 20
    |||||
Db 63 CTGCGATCCGACTCACCACAT 82

RESULT 8
LOCUS       CQ310858               555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION  Sequence 21963 from Patent WO0186003.
ACCESSION   CQ310858
VERSION     CQ310858.1 GI:41271435
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human lung
JOURNAL     Patent: WO 0186003-A 21963 15-NOV-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
            2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
            BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACCACAT 20
    |||||
Db 63 CTGCGATCCGACTCACCACAT 82

```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20
 Db 63 CTGCGATCCGACTCACC AAT 82

RESULT 9
 CQ347773
 LOCUS 555 bp DNA linear PAT 23-JAN-2004
 DEFINITION Sequence 21867 from Patent WO0157275.
 ACCESSION CQ347773
 VERSION CQ347773.1 GI:41296844
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 TITLE Human genome-derived single exon nucleic acid probes useful for
 analysis of gene expression in human brain
 JOURNAL Patent: WO 0157275-A 21867 09-AUG-2001;
 Aeomica, Inc. (US)

FEATURES
 source
 1..555
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
 1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-BST HUMAN HIT:
 BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
 0.00e+00"

ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 555;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20
 Db 63 CTGCGATCCGACTCACC AAT 82

RESULT 10
 CQ100639
 LOCUS 600 bp DNA linear PAT 21-JAN-2004
 DEFINITION Sequence 9498 from Patent WO0157272.
 ACCESSION CQ100639
 VERSION CQ100639.1 GI:41069665
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 TITLE Human genome-derived single exon nucleic acid probes useful for
 analysis of gene expression in human placenta
 JOURNAL Patent: WO 0157272-A 9498 09-AUG-2001;
 Aeomica, Inc. (US)

FEATURES
 source
 1..600
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
 0.99"

ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 600;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20
 Db 82 CTGCGATCCGACTCACC AAT 101

RESULT 11
 CQ139631
 LOCUS 600 bp DNA linear PAT 21-JAN-2004
 DEFINITION Sequence 9653 from Patent WO0157276.
 ACCESSION CQ139631
 VERSION CQ139631.1 GI:41097003
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 TITLE Human genome-derived single exon nucleic acid probes useful for
 analysis of gene expression in human bone marrow
 JOURNAL Patent: WO 0157276-A 9653 09-AUG-2001;
 Aeomica, Inc. (US)

FEATURES
 Location/Qualifiers
 1..600
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
 = 4.7"

ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 600;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20
 Db 82 CTGCGATCCGACTCACC AAT 101

RESULT 12
 CQ175964
 LOCUS 600 bp DNA linear PAT 21-JAN-2004
 DEFINITION Sequence 7360 from Patent WO0157274.
 ACCESSION CQ175964
 VERSION CQ175964.1 GI:41170703
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 TITLE Human genome-derived single exon nucleic acid probes useful for
 analysis of gene expression in human heart
 JOURNAL Patent: WO 0157274-A 7360 09-AUG-2001;
 Aeomica, Inc. (US)

FEATURES
 Location/Qualifiers
 1..600
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"

ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 600;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20
 Db 82 CTGCGATCCGACTCACC AAT 101

```

RESULT 13
CQ222999
LOCUS       CQ222999             600 bp    DNA          linear      PAT 21-JAN-2004
DEFINITION   Sequence 9838 from Patent WO0157273.
ACCESSION   CQ222999
VERSION      CQ222999.1  GI:41205280
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
              3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
              60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
              August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
              (03.10.00)<150> US 60/236,359<151> 27 September 2000
              (27.09.00)<150> US 60/234,687<151> 21 September 2000
              (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
              Molecular Dynamics Sequence Listing Engine
JOURNAL      Patent: WO 0157273-A 9838 09-AUG-2001;
              Asomica, Inc. (US)
FEATURES     source
              1..600
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
              = 1.7"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGATCCGACTCACCACAT 20
        |||||
Db      82 CTGGATCCGACTCACCACAT 101

RESULT 14
CQ260961
LOCUS       CQ260961             600 bp    DNA          linear      PAT 23-JAN-2004
DEFINITION   Sequence 9222 from Patent WO0157277.
ACCESSION   CQ260961
VERSION      CQ260961.1  GI:41233441
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER
JOURNAL      Patent: WO 0157277-A 9222 09-AUG-2001;
              Asomica, Inc. (US)
FEATURES     source
              1..600
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
              = 3.5"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGATCCGACTCACCACAT 20
        |||||
Db      82 CTGGATCCGACTCACCACAT 101

RESULT 15
CQ298444
LOCUS       CQ298444             600 bp    DNA          linear      PAT 23-JAN-2004
DEFINITION   Sequence 9549 from Patent WO0186003.
ACCESSION   CQ298444
VERSION      CQ298444.1  GI:41259021
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG
JOURNAL      Patent: WO 0186003-A 9549 15-NOV-2001;
              Asomica, Inc. (US)
FEATURES     source
              1..600
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL = 2"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGATCCGACTCACCACAT 20
        |||||
Db      82 CTGGATCCGACTCACCACAT 101

Search completed: February 4, 2005, 23:30:40
Job time : 482.738 secs

```

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169a-4

Perfect score: 20

Sequence: 1 ctgcgacgcactcaccacat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	AZ46974 Bcl-X1 MR
2	20	100.0	25	10	ADK66040 Standardi
3	20	100.0	337	10	ADK66037 Standardi
4	20	100.0	492	9	ACH46093 Human inf
5	20	100.0	555	4	ABA73433 Human foe
6	20	100.0	555	4	AAI53868 Probe #22
7	20	100.0	555	4	ABA38761 Probe #17
8	20	100.0	555	4	AAK48039 Human bon
9	20	100.0	555	4	AAK21876 Human bra
10	20	100.0	555	4	ABS47753 Human liv
11	20	100.0	555	6	ABS21972 Human gen
12	20	100.0	564	12	ACH87595 Human gen
13	20	100.0	600	4	ABA60917 Human foe
14	20	100.0	600	4	AAI40812 Probe #94
15	20	100.0	600	4	ABA28894 Probe #73
16	20	100.0	600	4	AAK35096 Human bon
17	20	100.0	600	4	AAK03207 Human bra
18	20	100.0	600	4	ABS34848 Human liv
19	20	100.0	600	6	ABS09558 Human gen
20	20	100.0	636	4	AAH48169 Mutant bc
21	20	100.0	702	5	AAH43464 cDNA clon

ALIGNMENTS

RESULT 1

AZ46974

ID AZ46974 standard; DNA; 20 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

CC lesions. They can also be included with a carrier (and optionally tetra
 CC meso-(4-methylpyridyl)porphine and/or tetra meso-(anilinium)porphine; in
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
 CC represent antisense oligos specific for the bcl-Xl mRNA

XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0

QY 1 CTGCGATCCGACTCACCACAT 20
 DB 1 CTGCGATCCGACTCACCACAT 20

RESULT 2
 ADK66040/c
 ID ADK66040 standard; DNA; 25 BP.
 XX
 AC ADK66040;
 DT 06-MAY-2004 (first entry)
 XX
 DE Standardized polynucleotide system polynucleotide #8 probe.
 XX
 KW ss; standardized polynucleotide system; medical diagnosis;
 KW functional genomics; sample analysis; pharmacogenomics; sample analysis;
 KW probe.
 XX
 OS Unidentified.
 XX
 PN DE10209071-A1.
 XX
 PD 25-SEP-2003.
 XX
 PF 28-FEB-2002; 2002DE-01009071.
 XX
 PR 28-FEB-2002; 2002DE-01009071.
 XX

PA (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
 XX
 PI Koehler T, Rost A;
 XX
 DR WPI; 2003-732912/70.
 XX

PT Standardized polynucleotide system, useful for quantitative, real-time
 PT determination of nucleic acid, comprises stabilized standards, primers
 PT and probe.
 XX
 PS Claim 1; Page 7; 38pp; German.
 XX
 CC The present invention relates to a standardized polynucleotide system,
 CC which comprises at least one carrier nucleic acid, at least 3
 CC oligonucleotides, as primers and target-specific, fluorescently labeled
 CC probe and optionally at least one set of stabilized controls (standard
 CC RNA or DNA) of known concentration and instructions. The system comprises
 CC any of 20 sets of one control, two primers and one target-specific probe.
 CC The standardized polynucleotide system can be used for quantitative, real
 CC -time detection of target nucleic acids, especially analysis of genes or
 CC gene products, e.g. for individualized medical diagnosis, in veterinary
 CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,
 CC pharmaceutical testing, analysis of food or environmental samples and
 CC also for ultra-sensitive detection of proteins by immuno-PCR. The present
 CC sequence is a probe used to isolate a polynucleotide used in the system
 CC of the invention.

XX Sequence 25 BP; 4 A; 4 C; 10 G; 7 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 10; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20
 DB 1 CTGCGATCCGACTCACCACAT 20

QY 1 CTGCGATCCGACTCACCACAT 20
 DB 20 CTGCGATCCGACTCACCACAT 1

RESULT 3
 ADK66037/c
 ID ADK66037 standard; DNA; 337 BP.
 XX
 AC ADK66037;
 DT 06-MAY-2004 (first entry)
 XX
 DE Standardized polynucleotide system polynucleotide #8.

XX ss; standardized polynucleotide system; medical diagnosis;
 KW functional genomics; sample analysis; pharmacogenomics; sample analysis.
 KW Unidentified.
 XX
 PN DE10209071-A1.
 XX
 PD 25-SEP-2003.
 XX
 PF 28-FEB-2002; 2002DE-01009071.
 XX
 PR 28-FEB-2002; 2002DE-01009071.
 XX

PA (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
 XX
 PI Koehler T, Rost A;
 XX
 DR WPI; 2003-732912/70.
 XX

PT Standardized polynucleotide system, useful for quantitative, real-time
 PT determination of nucleic acid, comprises stabilized standards, primers
 PT and probe.
 XX
 PS Claim 1; Page 7; 38pp; German.
 XX
 CC The present invention relates to a standardized polynucleotide system,
 CC which comprises at least one carrier nucleic acid, at least 3
 CC oligonucleotides, as primers and target-specific, fluorescently labeled
 CC probe and optionally at least one set of stabilized controls (standard
 CC RNA or DNA) of known concentration and instructions. The system comprises
 CC any of 20 sets of one control, two primers and one target-specific probe.
 CC The standardized polynucleotide system can be used for quantitative, real
 CC -time detection of target nucleic acids, especially analysis of genes or
 CC gene products, e.g. for individualized medical diagnosis, in veterinary
 CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,
 CC pharmaceutical testing, analysis of food or environmental samples and
 CC also for ultra-sensitive detection of proteins by immuno-PCR. The present
 CC sequence is a polynucleotide used in the system of the invention.

XX Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20
 DB 99 CTGCGATCCGACTCACCACAT 80

RESULT 4
 ACH46093/c
 ID ACH46093 standard; cDNA; 492 BP.
 XX
 AC ACH46093;
 DT 13-OCT-2003 (first entry)
 XX

```

DE Human infant brain cDNA #156.
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX Homo sapiens.
OS US2003073623-A1.
PN 17-APR-2003.
XX 30-JUL-2001; 2001US-00918995.
XX 30-JUL-2001; 2001US-00918995.
XX (DRMA//) DRMANAC R T.
PA (LABA//) LABAT I.
PA (STAC//) STACHE-CRAIN B.
PA (DICK//) DICKSON M C.
PA (JONE//) JONES L W.
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX Claim 1; SEQ ID NO 33305; 44pp; English.
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX SQ Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20
DB 283 CTGCGATCCGACTCACCACAT 264

RESULT 5
ABA73433
ID ABA73433 standard; DNA; 555 BP.
XX AC ABA73433;
XX DT 01-FEB-2002 (first entry)
XX DE Human foetal liver single exon nucleic acid probe #21738.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX

DE Human infant brain cDNA #156.
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX Homo sapiens.
OS WO200157277-A2.
PN 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000669.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human foetal liver.
XX Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20
DB 63 CTGCGATCCGACTCACCACAT 82

RESULT 6
AAI53868
ID AAI53868 standard; DNA; 555 BP.
XX AC AAI53868;
XX DT 17-OCT-2001 (first entry)
XX DE Probe #22554 used to measure gene expression in human placenta sample.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000663.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.

```

```
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 22554; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENPs).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCGATCCGACTCACC AAT 20
DB 63 CTGCGATCCGACTCACC AAT 82
RESULT 7
ABA38761
ID ABA38761 standard; DNA; 555 BP.
XX
XX ABA38761;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #1727 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 4; SEQ ID NO 1727; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC
```

```
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCGATCCGACTCACC AAT 20
DB 63 CTGCGATCCGACTCACC AAT 82
RESULT 8
AAK48039
ID AAK48039 standard; DNA; 555 BP.
XX
XX AAK48039;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 22596.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGATCCGACTCACCACAT 20
 Db 63 CTGGGATCCGACTCACCACAT 82

RESULT 9
 AAK21876
 ID AAK21876 standard; DNA; 555 BP.
 XX AC
 XX AAK21876;
 XX DT
 XX 05-NOV-2001 (first entry)
 XX DE Human brain expressed single exon probe SEQ ID NO: 21867.
 XX DE Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KW ss.
 XX OS Homo sapiens.
 XX OS WO200157275-A2.
 XX PN
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000667.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483446/52.
 XX DR Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 XX Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
 XX CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention
 XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGATCCGACTCACCACAT 20
 Db 63 CTGGGATCCGACTCACCACAT 82

RESULT 10
 ABS47753
 ID ABS47753 standard; DNA; 555 BP.
 XX AC
 XX ABS47753;
 XX DT
 XX 19-AUG-2002 (first entry)
 XX DE Human genome-derived single exon probe ORF from lung SEQ ID NO 21963.
 XX DE Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;

DT 25-FEB-2003 (first entry)
 XX Human liver single exon probe, SEQ ID No 22743.
 DE Human; single exon nucleic acid probe; liver; cirrhosis;
 XX hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 KW coronary heart disease; ss.
 XX OS Homo sapiens.
 XX OS WO200157273-A2.
 XX PN
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000664.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.
 XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX Claim 4; SEQ ID NO 22743; 658pp; English.
 XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human
 CC liver single exon nucleic acid probes of the invention. Note: The
 CC sequence information for this patent does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGATCCGACTCACCACAT 20
 Db 63 CTGGGATCCGACTCACCACAT 82

RESULT 11
 ABS21972
 ID ABS21972 standard; DNA; 555 BP.
 XX AC
 XX ABS21972;
 XX DT
 XX 19-AUG-2002 (first entry)
 XX DE Human genome-derived single exon probe ORF from lung SEQ ID NO 21963.
 XX DE Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenar syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
XX
OS Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 4; SEQ ID NO 21963; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karagenar syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a single exon probe open reading frame of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGATCCGACTCACCACAT 20
|||
DB 63 CTGGGATCCGACTCACCACAT 82
RESULT 12
ACH87595
ID ACH87595 standard; DNA; 564 BP.
XX
AC ACH87595;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon probe #20790.
XX
KW Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
XX US2003194704-A1.
XX
PD 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX (PENN/) PENN S G.
XX PA (RANK/) RANK D R.
XX PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX
XX Claim 1; SEQ ID NO 20790; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene

CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids, or
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGATCCGACTACCAAT 20
Dy 63 CTGGATCCGACTACCAAT 82

RESULT 13

ID ABA60917 standard; DNA; 600 BP.

AC ABA60917;

DT 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #9222.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS Homo sapiens.

XX WO200157277-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US0000669.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human foetal liver.

PS Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human foetal liver. The

XX present sequence is a single exon nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGATCCGACTACCAAT 20
Dy 82 CTGGATCCGACTACCAAT 101

RESULT 14

ID AAI40812 standard; DNA; 600 BP.

XX AAI40812;

DT 17-OCT-2001 (first entry)

DE Probe #9498 used to measure gene expression in human placenta sample.

XX Probe; microarray; human; placenta; antenatal diagnosis;

XX genetic disorder; ss.

OS Homo sapiens.

XX WO200157272-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US0000663.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

PS Claim 25; SEQ ID NO 9498; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).

XX The present sequence is one such probe. The probes are useful for

XX producing a microarray for predicting, measuring and displaying gene

XX expression in samples derived from human placenta. The probes are useful

XX for antenatal diagnosis of human genetic disorders

XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 600;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGATCCGACTACCAAT 20

Dy 82 CTGGATCCGACTACCAAT 101

RESULT 15

ABA28894

ID ABA28894 standard; DNA; 600 BP.

XX ABA28894;

XX ABA28894;

DT 23-JAN-2002 (first entry)
XX
DE Probe #7360 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 1; SEQ ID NO 7360; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCAT 20
|||||
Db 82 CTGCGATCCGACTCACCAT 101

Search completed: February 4, 2005, 21:52:41
Job time : 259.033 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-4
Perfect score: 20
Sequence: 1 ctgcgatccactcaacaaat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	167	4	BM820203
C 2	20	100.0	332	2	AW820481
C 3	20	100.0	396	4	BM818649
C 4	20	100.0	418	4	BT051278
C 5	20	100.0	437	7	W01420
C 6	20	100.0	447	4	BM818387
C 7	20	100.0	456	8	AZ537061
C 8	20	100.0	478	2	BM050133
C 9	20	100.0	485	2	AW814883
C 10	20	100.0	555	2	BE393580
C 11	20	100.0	563	2	BE617040
C 12	20	100.0	579	4	BM741157
C 13	20	100.0	620	4	BM820164
C 14	20	100.0	657	2	BE207063
C 15	20	100.0	681	6	CF147016
C 16	20	100.0	687	2	BE293685
C 17	20	100.0	695	4	BI252492
C 18	20	100.0	697	4	BI457116
C 19	20	100.0	699	2	BE870269
C 20	20	100.0	700	4	BG831301
C 21	20	100.0	705	4	BG290422
C 22	20	100.0	711	2	BE535474
C 23	20	100.0	714	4	BG470667
C 24	20	100.0	798	5	BU528551

C 25	20	100.0	798	7	CK000319
C 26	20	100.0	808	4	BI222971
C 27	20	100.0	818	4	BG824757
C 28	20	100.0	830	7	CF619432
C 29	20	100.0	836	4	BM018295
C 30	20	100.0	843	5	BQ962018
C 31	20	100.0	845	5	BU527940
C 32	20	100.0	859	6	CD359906
C 33	20	100.0	860	1	AL537680
C 34	20	100.0	872	5	BU168531
C 35	20	100.0	874	5	BU844419
C 36	20	100.0	878	5	BQ888053
C 37	20	100.0	882	5	BQ646768
C 38	20	100.0	901	5	BQ940282
C 39	20	100.0	912	5	BQ935725
C 40	20	100.0	919	5	BQ948029
C 41	20	100.0	920	5	BQ646527
C 42	20	100.0	920	5	BU528504
C 43	20	100.0	922	5	BQ924197
C 44	20	100.0	923	5	BQ927754
C 45	20	100.0	925	4	BM018845

ALIGNMENTS

RESULT 1
BM820203/c
LOCUS BM820203 167 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0089575 S20T665307 Homo sapiens cDNA clone S20T665307-9-G04
S., mRNA sequence.
ACCESSION BM820203
VERSION BM820203.1 GI:19176616
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 167)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yusong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 9 row: G column: 04
High quality sequence stop: 167.
Location/Qualifiers
1. .167
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-9-G04"
/sex="M"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pcNS; Site 1: EcorI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including Ecor
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcorI which site is also included in vector. An RNA strand

FEATURES
source

converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 CTGCGATCCGACTCACCACAT 20
|||||
Db 136 CTGCGATCCGACTCACCACAT 117

RESULT 2

AW820481/c
LOCUS
DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW820481
VERSION AW820481.1 GI:7913475
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 332)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,D.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
MEDLINE
PUBMED
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=st2=QV2-ST0298-140200-042-f12&t3=2000-02-14&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 332.

FEATURES

source

1..332
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ST0298"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20
|||||
Db 103 CTGCGATCCGACTCACCACAT 84

RESULT 3

BM818649/c
LOCUS
DEFINITION K-BST0085991 S20T665307 Homo sapiens cDNA clone S20T665307-4-F03 5', mRNA sequence.

ACCESSION BM818649
VERSION BM818649.1 GI:19175062
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: F column: 03
High quality sequence stop: 396.

TITLE
JOURNAL
COMMENT
Location/Qualifiers
1..396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-4-F03"
/sex="M"
/lab_host="Top10F"
/clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pcns; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including BcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

100.0%; Score 20; DB 4; Length 396;
Query Match 100.0%; Pred. No. 7.8; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 CTGCGATCCGACTCACCACAT 20
|||||
Db 136 CTGCGATCCGACTCACCACAT 117

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.8; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 CTGCGATCCGACTCACCACAT 20
|||||
Db 136 CTGCGATCCGACTCACCACAT 117

RESULT 4

BI051278
LOCUS
DEFINITION CM3-GN0297-110101-607-f03 GN0297 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI051278

VERSION BI051278.1 GI:14459808
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 418)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&tl2=CM3-GN0297-110101-607-f03&tl3=2001-01-11&tl4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 3
 High quality sequence stop: 418.
 FEATURES
 Location/Qualifiers
 source 1..418
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="GN0297"
 /note="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 ORIGIN
 Query Match 100.0%; Score 20; DB 4; Length 418;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTGGATCCGACTCACCACAT 20
 |||||
 Db 223 CTGGATCCGACTCACCACAT 242
 RESULT 5
 W01420/c
 LOCUS
 DEFINITION W01420.1 Soares fetal lung NbHL19W Homo sapiens cDNA clone
 IMAGE:298187 5' similar to SW:BCIX_HUMAN Q07817 APOPTOSIS REGULATOR
 BCL-X., mRNA sequence.
 W01420
 ACCESSION W01420.1 GI:1273428
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 437)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Contact: Wilson RK
 Unpublished (1995)
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: mob.REGA+ET
 High quality sequence stop: 383.
 FEATURES
 Location/Qualifiers
 source 1..437
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:1243109"
 /db_xref="taxon:9606"
 /clone="IMAGE:298187"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal_lung NbHL19W"
 /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCATCTGAAGTGGAGCGCGCAATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library. Soares fetal heart NbHL19W."
 ORIGIN
 Query Match 100.0%; Score 20; DB 7; Length 437;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTGGATCCGACTCACCACAT 20
 |||||
 Db 258 CTGGATCCGACTCACCACAT 239
 RESULT 6
 BM818387/c
 LOCUS
 DEFINITION K-EST0085558 S20T665307 Homo sapiens cDNA clone S20T665307-3-B02
 5', mRNA sequence.
 BM818387
 ACCESSION BM818387.1 GI:19174800
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 447)
 REFERENCE Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr
 Plate: 3 Row: B Column: 02
 High quality sequence stop: 447.

FEATURES

source
 Location/Qualifiers
 1. .447
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S20T665307-3-B02"
 /sex="M"
 /lab_host="Top10F"
 /clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 447;
 Best Local Similarity 100.0%; Pred. No. 7.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0

QY 1 CTGCGATCCGACTCACCACAT 20
 Db 136 CTGCGATCCGACTCACCACAT 117

RESULT 7

AZ537061
 LOCUS
 DEFINITION
 AZ537061 456 bp DNA linear GSS 06-NOV-2000
 AST-2P01514 AB Genetrap PC-3 Human Prostatic Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M., Bernardino,A., Durick,K. and Pollok,B.
 Exon-trap tags from a PC-3 Genomescreen(TM) Library
 Unpublished (2000)

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Greg Henkel
 Gene Expression
 Aurora Biosciences Corp.
 11010 Torreyana Road, San Diego, CA 92121, USA
 Tel: 8584048436
 Fax: 8584046719
 Email: henkel@aurorabio.com

Pools of cells were isolated from a Genomescreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase preceded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAMP-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.

Class: exon-trapped.

Location/Qualifiers
 1. .456
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /tissue_type="Adenocarcinoma"
 /cell_type="Epithelial"
 /clone_lib="Genetrap PC-3 Human Prostatic Carcinoma Library"
 /note="Organ: Prostate; Vector: pAMP-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAMP-1 and used to transform DH5-alpha competent bacteria."

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 456;
 Best Local Similarity 100.0%; Pred. No. 7.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0

QY 1 CTGCGATCCGACTCACCACAT 20
 Db 194 CTGCGATCCGACTCACCACAT 213

RESULT 8

BM050133/c
 LOCUS
 DEFINITION
 BM050133 478 bp mRNA linear EST 07-NOV-2001
 603632480F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5422338 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 478)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1879 row: p column: 19
 High quality sequence stop: 267.

FEATURES

source
 Location/Qualifiers
 1. .478
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5422338"
 /tissue_type="epithelioid carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_42"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 478;

Best Local Similarity 100.0%; Pred. No. 7.9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACCACAT 20
Db 242 CTGCGATCCGACTCACCACAT 223

RESULT 9

AW814883

LOCUS

DEFINITION MR1-ST0206-120400-022-f04 ST0206 Homo sapiens CDNA, mRNA linear EST 17-MAY-2000

ACCESSION

AW814883

VERSION

AW814883.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 486)

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F.F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

PUBMED

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-mr1-ST0206-120400-022-f04&t3=2000-04-12&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 55

High quality sequence stop: 485.

FEATURES

Location/Qualifiers

1..486

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev stage="Adult"

/clone_lib="ST0206"

/note="Organ: stomach; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 7.9;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACCACAT 20

Db 185 CTGCGATCCGACTCACCACAT 204

RESULT 10

BE393580/c

LOCUS

DEFINITION

601310279F1 NIH_MGC_44 Homo sapiens CDNA clone IMAGE:3632058 5', mRNA sequence.

ACCESSION

BE393580

VERSION

BE393580.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 555)

AUTHORS

NTH-MGC http://mgc.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LICM322 row: m column: 19

High quality sequence stop: 551.

FEATURES

Location/Qualifiers

1..555

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="NIH MGC 44"

/tissue_type="endometrium, adenocarcinoma cell line"

/lab host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCM87; Site: 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACCACAT 20

Db 71 CTGCGATCCGACTCACCACAT 52

RESULT 11

BE617040/c

LOCUS

DEFINITION

601441454F1 NIH_MGC_65 Homo sapiens CDNA clone IMAGE:3845892 5', mRNA sequence.

ACCESSION

BE617040

VERSION

BE617040.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 563)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Arranged by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM9557 row: k column: 13
 High quality sequence stop: 561.

FEATURES

Location/Qualifiers

1..563
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3845892"
 /tissue_type="adenocarcinoma"
 /lab_host="DH108 (phage-resistant)"
 /clone_lib="NIH_MGC_65"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies." source

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 563;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20

Db 37 CTGCGATCCGACTCACCACAT 18

RESULT 12

BM741157/c

LOCUS BM741157 579 bp mRNA linear EST 01-MAR-2002
 DEFINITION K-EST0013545 S6SNU620 Homo sapiens cDNA clone S6SNU620-6-A10 5',
 mRNA sequence.

ACCESSION BM741157.1 GI:19062486

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 579)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 6 row: A column: 10

High quality sequence stop: 579.

Location/Qualifiers

1..579

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S6SNU620-6-A10"

/sex="F"

/tissue_type="Ascites"

/cell_type="Scattering floating"

/cell_line="SNU-620"

/lab_host="Top10F"

/clone_lib="S6SNU620"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 579;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20

Db 164 CTGCGATCCGACTCACCACAT 145

RESULT 13

BM820164/c

LOCUS BM820164 620 bp mRNA linear EST 06-MAR-2002
 DEFINITION K-EST0089533 S20T65307 Homo sapiens cDNA clone S20T65307-9-C10
 5', mRNA sequence.

ACCESSION BM820164

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 620)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 9 row: C column: 10

High quality sequence stop: 620.

Location/Qualifiers

1..620

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S20T65307-9-C10"

/sex="M"

/lab_host="Top10F"

/clone_lib="S20T65307"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.

```

The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 620;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACC AAT 20
    |||||
Db 136 CTGCGATCCGACTCACC AAT 117

RESULT 14
BE207063/c
LOCUS
DEFINITION
ba09f05.y1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2823873 5'
similar to gb:L35049 Mus musculus Bcl-XL mRNA, complete cds
(MOUSE);, mRNA sequence.

ACCESSION
BE207063
VERSION
BE207063.1 GI:8750461
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Other ESTs: ba09f05.x1
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library
Arranged by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 450.

FEATURES
source
1..657
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2823873"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 657;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACC AAT 20
    |||||
Db 533 CTGCGATCCGACTCACC AAT 514

RESULT 15
CF147016/c
LOCUS
```

```

DEFINITION
UI-HF-CB0-atf-g-11-0-UI.r1 NIH_MGC 210 Homo sapiens cDNA clone
IMAGE:30570802 5', mRNA sequence.

ACCESSION
CF147016
VERSION
CF147016.1 GI:33262460
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bonaldo,M.F., Lennon,G. and Soares,M.B.
AUTHORS
Normalization and subtraction: two approaches to facilitate gene
discovery
TITLE
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Tim Ratliff
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pYX-5.

FEATURES
source
1..681
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30570802"
/tissue_type="CNCAP(3)T-225 cell line"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_MGC 210"
/notes="Organ: Prostate; Vector: pT7T3 Pac; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pT7T3 Pac vector. The library tag
sequence located between the Not I site and the polyA tail
is CCCAC. Tissue was provided by Tim Ratliff."
```

```

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 681;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACC AAT 20
    |||||
Db 38 CTGCGATCCGACTCACC AAT 19
```

```

Search completed: February 5, 2005, 08:11:37
Job time : 2390.67 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-5
Perfect score: 18
Sequence: 1 agtcctgttcttccac 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644845745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235153
2	18	100.0	18	6	BD235168
3	18	100.0	512	6	CQ727769
4	18	100.0	555	6	CQ113695
5	18	100.0	555	6	CQ152574
6	18	100.0	555	6	CQ185831
7	18	100.0	555	6	CQ235904
8	18	100.0	555	6	CQ273477
9	18	100.0	555	6	CQ310858
10	18	100.0	555	6	CQ347773
11	18	100.0	600	6	CQ106639
12	18	100.0	600	6	CQ139631
13	18	100.0	600	6	CQ175964
14	18	100.0	600	6	CQ222999
15	18	100.0	600	6	CQ260961
16	18	100.0	600	6	CQ298444
17	18	100.0	600	6	CQ335104
18	18	100.0	636	6	BD097037
19	18	100.0	702	4	AY005131

c 20	18	100.0	702	6	BD084108
c 21	18	100.0	702	6	BD102202
c 22	18	100.0	702	9	BT007208
c 23	18	100.0	702	12	BT008248
c 24	18	100.0	723	9	HSU72398
c 25	18	100.0	737	6	AR054022
c 26	18	100.0	737	6	AR172595
c 27	18	100.0	737	6	IS2012
c 28	18	100.0	737	6	AR371662
c 29	18	100.0	737	6	AR380913
c 30	18	100.0	737	9	HSBCLXS
c 31	18	100.0	747	6	AX127722
c 32	18	100.0	926	6	AR054021
c 33	18	100.0	926	6	AR118504
c 34	18	100.0	926	6	AR124952
c 35	18	100.0	926	6	AR144311
c 36	18	100.0	926	6	AR172594
c 37	18	100.0	926	6	BD243042
c 38	18	100.0	926	6	CQ765842
c 39	18	100.0	926	6	E58777
c 40	18	100.0	926	6	IS2011
c 41	18	100.0	926	6	AR371661
c 42	18	100.0	926	6	AR380885
c 43	18	100.0	926	6	AX839772
c 44	18	100.0	926	6	AX925686
c 45	18	100.0	926	9	HSBCLXL

ALIGNMENTS

RESULT 1
BD235153
LOCUS BD235153 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION BD235153
VERSION BD235153.1 GI:33044923
KEYWORDS JP 2002519048-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Stein, C.A.
TITLE Oligonucleotide inhibitors of bcl-xL
JOURNAL Patent: JP 2002519048-A 5 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT OS Artificial Sequence
PN JP 2002519048-A/5
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN
PC C12N15/09, A61K9/127, A61K31/711, A61K31/712, A61K31/7125, PC A61K47/42,
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..18 /organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTCCTGTCTCTTCCAC 18
|||||

```
Db      1 AGTCCTGTTCTCTCCAC 18

RESULT 2
LOCUS      BD235168                18 bp    DNA          linear    PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235168
VERSION    BD235168.1 GI:33044938
KEYWORDS   JP 2002519048-A/20.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 20 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/20
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC
           C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125,PC
           A61K47/42,
           PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
           CC ANTISENSE OLIGONUCLEOTIDE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           FT Key Location/Qualifiers
           FT misc binding (1)..(6)
           FT misc binding (8)..(9)
           FT misc binding (10)..(12)
           FT misc binding (13)..(18).
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"

FEATURES             source
   source            1..18
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTCCTGTTCTCTCCAC 18
      |||||
Db      1 AGTCCTGTTCTCTCCAC 18

RESULT 3
LOCUS      CQ727769/c              512 bp    DNA          linear    PAT 03-FEB-2004
DEFINITION Sequence 13703 from Patent WO02068579.
ACCESSION  CQ727769
VERSION    CQ727769.1 GI:42294740
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE      Kits, such as nucleic acid arrays, comprising a majority of
           humanexons or transcripts, for detecting expression and other uses
           thereof
JOURNAL    Patent: WO 02068579-A 13703 06-SEP-2002;
           PE Corporation (NY) (US)
           Location/Qualifiers

FEATURES             source
   source            1..555
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTCCTGTTCTCTCTCCAC 18
      |||||
Db      460 AGTCCTGTTCTCTCTCCAC 477

RESULT 5
LOCUS      CQ152574                555 bp    DNA          linear    PAT 21-JAN-2004
DEFINITION Sequence 22596 from Patent WO0157276.
ACCESSION  CQ152574
VERSION    CQ152574.1 GI:41159924
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human bone marrow
JOURNAL    Patent: WO 0157276-A 22596 09-AUG-2001;
           Aeomica, Inc. (US)
           Location/Qualifiers

FEATURES             source
   source            1..555
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTCCTGTTCTCTCTCCAC 18
      |||||
Db      460 AGTCCTGTTCTCTCTCCAC 477

RESULT 4
LOCUS      CQ113695                555 bp    DNA          linear    PAT 21-JAN-2004
DEFINITION Sequence 22554 from Patent WO0157272.
ACCESSION  CQ113695
VERSION    CQ113695.1 GI:41083565
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human placenta
JOURNAL    Patent: WO 0157272-A 22554 09-AUG-2001;
           Aeomica, Inc. (US)
           Location/Qualifiers

FEATURES             source
   source            1..555
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"
   /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
           0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
           HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
           0.00e+00"
```

/db xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 4.7-SWISSPROT HIT: Q07817, EVALUATION 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUATION 0.00e+00-NT HIT: U72398.1, EVALUATION
0.00e+00"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTCCAC 18

|||||
Db 460 AGTCCTGTTCTCTCCAC 477

RESULT 6

LOCUS CQ185831 555 bp DNA linear PAT 21-JAN-2004

DEFINITION Sequence 17227 from Patent WO0157274.

ACCESSION CQ185831

VERSION CQ185831.1 GI:41180846

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

Human genome-derived single exon nuclear acid probes useful for
analysis of gene expression in human heart

Patent: WO 0157274-A 17227 09-AUG-2001;

Aeomica, Inc. (US)

FEATURES

source Location/Qualifiers

1..555

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =

1.4-SWISSPROT HIT: Q07817, EVALUATION 1.00e-106-EST HUMAN HIT:

BE207063.1, EVALUATION 0.00e+00-NT HIT: U72398.1, EVALUATION

0.00e+00"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTCCAC 18

|||||
Db 460 AGTCCTGTTCTCTCCAC 477

RESULT 7

LOCUS CQ235904 555 bp DNA linear PAT 21-JAN-2004

DEFINITION Sequence 22743 from Patent WO0157273.

ACCESSION CQ235904

VERSION CQ235904.1 GI:41219182

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO

3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US

60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03

August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000

(03.10.00)<150> US 60/236,359<151> 27 September 2000

(27.09.00)<150> US 60/234,687<151> 21 September 2000

(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 22743 09-AUG-2001;
Aeomica, Inc. (US)

FEATURES

source Location/Qualifiers

1..555

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL

= 1.7-SWISSPROT HIT: Q07817, EVALUATION 1.00e-106-EST HUMAN

HIT: BE207063.1, EVALUATION 0.00e+00-NT HIT: U72398.1, EVALUATION

0.00e+00"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 555;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTCCAC 18

|||||
Db 460 AGTCCTGTTCTCTCCAC 477

RESULT 8

LOCUS CQ273477 555 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 21738 from Patent WO0157277.

ACCESSION CQ273477

VERSION CQ273477.1 GI:41246081

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

Human genome-derived single exon nuclear acid probes useful for
analysis of gene expression in human fetal liver

Patent: WO 0157277-A 21738 09-AUG-2001;

Aeomica, Inc. (US)

FEATURES

source Location/Qualifiers

1..555

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL

= 3.5-SWISSPROT HIT: Q07817, EVALUATION 1.00e-106-EST HUMAN

HIT: BE207063.1, EVALUATION 0.00e+00-NT HIT: U72398.1, EVALUATION

0.00e+00"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTCCAC 18

|||||
Db 460 AGTCCTGTTCTCTCCAC 477

RESULT 9

LOCUS CQ310858 555 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 21963 from Patent WO0186003.

ACCESSION CQ310858

VERSION CQ310858.1 GI:41271435

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
|||||
Db 460 AGTCCTGTTCTCTTCCAC 477

RESULT 10
LOCUS Q0347773 555 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21867 from Patent WO0157275.
ACCESSION Q0347773
VERSION Q0347773.1 GI:41296844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
|||||
Db 460 AGTCCTGTTCTCTTCCAC 477

RESULT 11
LOCUS Q0100639 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 9498 from Patent WO0157272.
ACCESSION Q0100639
VERSION Q0100639.1 GI:41069665
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
|||||
Db 479 AGTCCTGTTCTCTTCCAC 496

RESULT 12
LOCUS Q0139631 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 9653 from Patent WO0157276.
ACCESSION Q0139631
VERSION Q0139631.1 GI:41097003
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 4.7"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
|||||
Db 479 AGTCCTGTTCTCTTCCAC 496

RESULT 13
LOCUS Q0175964 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 7360 from Patent WO0157274.
ACCESSION Q0175964
VERSION Q0175964.1 GI:41170703
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 4.7"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
|||||
Db 479 AGTCCTGTTCTCTTCCAC 496

analysis of gene expression in human heart
Patent: WO 0157274-A 7360 09-AUG-2001;
Aeomica, Inc. (US)
JOURNAL
FEATURES
source
1. .600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 479 AGTCCTGTTCTCTCCAC 496

RESULT 14
CQ222999
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS
TITLE
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 9838 09-AUG-2001;
Aeomica, Inc. (US)
JOURNAL
FEATURES
source
1. .600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
= 1.7"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 479 AGTCCTGTTCTCTCCAC 496

RESULT 15
CQ260961
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS
TITLE
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 9838 09-AUG-2001;
Aeomica, Inc. (US)
JOURNAL
FEATURES
source
1. .600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
= 3.5"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 479 AGTCCTGTTCTCTCCAC 496

Search completed: February 4, 2005, 23:30:40
Job time : 432.664 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169a-5
Perfect score: 18
Sequence: 1 agtcctgtctcttcac 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	Az46975 Bcl-Xl mr
2	18	100.0	555	4	Aba73433 Human foe
3	18	100.0	555	4	Aa153868 Probe #22
4	18	100.0	555	4	Aba38761 Probe #17
5	18	100.0	555	4	Aak48039 Human bon
6	18	100.0	555	4	Aak21876 Human bra
7	18	100.0	555	4	Abs47753 Human liv
8	18	100.0	555	6	Abs21972 Human gen
9	18	100.0	559	12	Ach73889 Human gen
10	18	100.0	564	12	Ach87595 Human gen
11	18	100.0	600	4	Aba60917 Human foe
12	18	100.0	600	4	Aa140812 Probe #94
13	18	100.0	600	4	Aba28894 Probe #73
14	18	100.0	600	4	Aak35096 Human bon
15	18	100.0	600	4	Aak09207 Human bra
16	18	100.0	600	4	Abs34848 Human liv
17	18	100.0	600	6	Abs09558 Human gen
18	18	100.0	636	4	Aah48169 Mutant bc
19	18	100.0	702	5	Aah43464 cDNA clon
20	18	100.0	702	12	Adm45994 Human apo
21	18	100.0	737	2	Aaq81699 Human thy

c	22	18	100.0	737	10	AB283507
c	23	18	100.0	737	11	AD132132
c	24	18	100.0	739	12	ADG65218
c	25	18	100.0	747	4	AAF30926
c	26	18	100.0	747	12	ADG65209
c	27	18	100.0	926	2	AAQ81698
c	28	18	100.0	926	2	AAQ10079
c	29	18	100.0	926	3	AAZ93614
c	30	18	100.0	926	4	AAZ93614
c	31	18	100.0	926	4	AAZ93614
c	32	18	100.0	926	4	AAZ93614
c	33	18	100.0	926	6	ABK84766
c	34	18	100.0	926	8	ABT16641
c	35	18	100.0	926	10	AD56779
c	36	18	100.0	926	10	AD56779
c	37	18	100.0	926	11	AD56779
c	38	18	100.0	926	12	ADH52630
c	39	18	100.0	926	12	ADH52630
c	40	18	100.0	926	12	ADH52630
c	41	18	100.0	1236	5	AA00247
c	42	18	100.0	1455	5	AA00247
c	43	18	100.0	2386	10	ADG89403
c	44	18	100.0	2386	12	ADN04260
c	45	18	100.0	2575	12	AD019866
c	46	18	100.0	7372	2	AAZ33182

ALIGNMENTS

RESULT 1

AAZ46975
ID AAZ46975 standard; DNA; 18 BP.

XX AAZ46975;

DT 14-APR-2000 (first entry)

XX Bcl-Xl mRNA specific antisense oligo E.

XX Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;
XX lung; bladder; bcl-2; vascular lesion; antisense; ss.

XX Homo sapiens.

XX WC200001393-A2.

PD 13-JAN-2000.

XX 02-JUL-1999; 99WO-US015250.

XX 02-JUL-1998; 98US-00109614.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Stein CA;

XX WPI; 2000-137140/12.

XX New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

XX Claim 1; Fig 1; 69pp; English.

XX The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
 CC represent antisense oligos specific for the bcl-Xl mRNA

XX Sequence 18 BP; 2 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
 |||||
 Db 1 AGTCCTGTTCTCTTCCAC 18

RESULT 2
 ABA73433
 ID ABA73433 standard; DNA; 555 BP.
 XX AC ABA73433;
 XX DT 01-FEB-2002 (first entry)
 XX DE Human foetal liver single exon nucleic acid probe #21738.
 XX KW Human, foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX OS Homo sapiens.
 XX PN WO200157277-A2.
 XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX PS Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/published_sequences
 XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
 |||||
 Db 460 AGTCCTGTTCTCTTCCAC 477

RESULT 3
 AAI53868
 ID AAI53868 standard; DNA; 555 BP.
 XX AC AAI53868;
 XX DT 17-OCT-2001 (first entry)
 XX DE Probe #22554 used to measure gene expression in human placenta sample.
 XX KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder; ss.
 XX OS Homo sapiens.
 XX PN WO200157272-A2.
 XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX PS Claim 25; SEQ ID NO 22554; 654pp; English.
 XX CC The present invention relates to single exon nucleic acid probes (SENP).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders
 XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
 |||||
 Db 460 AGTCCTGTTCTCTTCCAC 477

RESULT 4
 ABA38761
 ID ABA38761 standard; DNA; 555 BP.
 XX AC ABA38761;
 XX DT 23-JAN-2002 (first entry)
 XX DE Probe #17227 for gene expression analysis in human heart cell sample.
 XX KW Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.


```
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 4; SEQ ID NO 17227; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTCCTGTTCTCTCCAC 18
Db |||||
460 AGTCCTGTTCTCTCCAC 477
RESULT 5
AAK48039
ID AAK48039 standard; DNA; 555 BP.
XX
XX AAK48039;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 22596.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Claim 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTCCTGTTCTCTCCAC 18
Db |||||
460 AGTCCTGTTCTCTCCAC 477
RESULT 6
AAK21876
ID AAK21876 standard; DNA; 555 BP.
XX
XX AAK21876;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 21867.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
```

XX Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.

PS The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

CC epilepsy and cancers. The present sequence is one of the probes of the

CC invention

XX

XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1 AGTCCTGTTCTCTTCCAC 18

|||||

DB 460 AGTCCTGTTCTCTTCCAC 477

|||||

RESULT 7

ABS47753

ID ABS47753 standard; DNA; 555 BP.

XX

AC ABS47753;

XX

XX 25-FEB-2003 (first entry)

XX

DE Human liver single exon probe, SEQ ID No 22743.

XX

XX Human; single exon nucleic acid probe; liver; cirrhosis;

KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;

KW coronary heart disease; ss.

XX

XX Homo sapiens.

OS

XX WO200157273-A2.

PN

XX 09-AUG-2001.

PD

XX 30-JAN-2001; 2001WO-US000664.

PF

XX 04-FEB-2000; 2000US-0180312P.

PR

XX 26-MAY-2000; 2000US-0207456P.

PR

XX 30-JUN-2000; 2000US-00608408.

PR

XX 03-AUG-2000; 2000US-00632366.

PR

XX 21-SEP-2000; 2000US-0234687P.

PR

XX 27-SEP-2000; 2000US-0236359P.

PR

XX 04-OCT-2000; 2000GB-00024263.

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA

XX Penn SG, Hanzel DK, Chen W, Rank DR;

PI

XX WPI; 2001-488998/53.

DR

XX

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human adult liver.

PT

XX

XX Claim 4; SEQ ID NO 22743; 658pp; English.

PS

XX

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for

CC measuring human gene expression in a sample derived from human adult

CC liver, comprising one of 13109 defined nucleotide sequences given in the

CC specification (or complements/ fragments). The probe hybridises at high

CC stringency to a nucleic acid molecule expressed in the human adult liver.

CC (i) may be used for predicting, measuring and displaying gene expression

CC in samples derived from human adult liver. The genes identified may be

CC involved in genetic liver diseases such as cirrhosis,

CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is

CC associated with coronary heart disease. ABS25011-ABS51005 represent human

CC

CC liver single exon nucleic acid probes of the invention. Note: The

CC sequence information for this patent does not appear in the printed

CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1 AGTCCTGTTCTCTTCCAC 18

|||||

DB 460 AGTCCTGTTCTCTTCCAC 477

|||||

RESULT 8

ABS21972

ID ABS21972 standard; DNA; 555 BP.

XX

AC ABS21972;

XX

XX 19-AUG-2002 (first entry)

DT

XX

DE Human genome-derived single exon probe ORF from lung SEQ ID No 21963.

DE

XX

XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;

KW chronic obstructive pulmonary disease; interstitial lung disease;

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioliomyomatosis; Karagener syndrome;

KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease; open reading frame; ORF.

XX

XX Homo sapiens.

OS

XX WO200186003-A2.

PN

XX 15-NOV-2001.

PD

XX 30-JAN-2001; 2001WO-US000665.

PF

XX 04-FEB-2000; 2000US-0180312P.

PR

XX 26-MAY-2000; 2000US-0207456P.

PR

XX 30-JUN-2000; 2000US-00608408.

PR

XX 03-AUG-2000; 2000US-00632366.

PR

XX 21-SEP-2000; 2000US-0234687P.

PR

XX 27-SEP-2000; 2000US-0236359P.

PR

XX 04-OCT-2000; 2000GB-00024263.

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA

XX Penn SG, Hanzel DK, Chen W, Rank DR;

PI

XX WPI; 2002-114183/15.

DR

XX

XX Spatially-addressable set of single exon nucleic acid probes, used to

PT measure gene expression in human lung samples.

PT

XX

XX Claim 4; SEQ ID NO 21963; 634pp; English.

PS

XX

XX The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived

CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their

CC complements or the 12387 open reading frames derived from the 12614

CC probes. Also included are a microarray comprising the novel set of probes

CC ; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample

CC derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC

CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a single exon probe open reading frame of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 555;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
 |||||
 Db 460 AGTCCTGTTCTCTTCCAC 477

RESULT 9

ACH73889
 ID ACH73889 standard; DNA; 559 BP.

XX ACH73889;

AC ACH73889;

XX 29-JUL-2004 (first entry)

DE Human genome derived single exon probe #7084.

XX Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.

XX Homo sapiens.

PN US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for
 XX surveying tissues.

PS Claim 15; SEQ ID NO 7084; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expressions, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above). The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The present sequence is a human
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

SQ Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 559;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18

|||||

Db 55 AGTCCTGTTCTCTTCCAC 72

RESULT 10

ACH87595

ID ACH87595 standard; DNA; 564 BP.

XX ACH87595;

AC ACH87595;

XX 29-JUL-2004 (first entry)

DE Human genome derived single exon probe #20790.

XX Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.

XX Homo sapiens.

OS US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

```
PR 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX Claim 1; SEQ ID NO 20790; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 688 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
Db 460 AGTCCTGTTCTCTTCCAC 477
|||||
|||||

RESULT 11
ABA60917
ID ABA60917 standard; DNA; 600 BP.
XX
XX ABA60917;
AC
XX
XX 01-FEB-2002 (first entry)
DT
XX
XX Human foetal liver single exon nucleic acid probe #9222.
DE

PR 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX Claim 1; SEQ ID NO 20790; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 688 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
Db 460 AGTCCTGTTCTCTTCCAC 477
|||||
|||||

RESULT 11
ABA60917
ID ABA60917 standard; DNA; 600 BP.
XX
XX ABA60917;
AC
XX
XX 01-FEB-2002 (first entry)
DT
XX
XX Human foetal liver single exon nucleic acid probe #9222.
DE
```

```
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human foetal liver.
XX PS Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human foetal liver. The
XX present sequence is a single exon nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
Db 479 AGTCCTGTTCTCTTCCAC 496
|||||
|||||

RESULT 12
AAI40812
ID AAI40812 standard; DNA; 600 BP.
XX
XX AAI40812;
XX
XX 17-OCT-2001 (first entry)
DT
XX
XX Probe #9498 used to measure gene expression in human placenta sample.
DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX
```

```

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-006232366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PI WPI; 2001-488997/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 25; SEQ ID NO 9498; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AGTCCTGTTCTCTCCAC 18
Db ||||| ||||| ||||| |||||
479 AGTCCTGTTCTCTCCAC 496
XX
RESULT 13
ABA28894
ID ABA28894 standard; DNA; 600 BP.
XX
AC ABA28894;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #7360 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PI WPI; 2001-488999/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 1; SEQ ID NO 7360; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AGTCCTGTTCTCTCCAC 18
Db ||||| ||||| ||||| |||||
479 AGTCCTGTTCTCTCCAC 496
XX
RESULT 14
AAK35096
ID AAK35096 standard; DNA; 600 BP.
XX
AC AAK35096;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PI WPI; 2001-488990/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

```

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 479 AGTCCTGTTCTCTCCAC 496

RESULT 15

AAK09207
ID AAK09207 standard; DNA; 600 BP.

XX AC AAK09207;

XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe SEQ ID NO: 9198.

XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.

XX OS Homo sapiens.

XX PN WC200157275-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000667.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-483446/52.

XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX brains.

XX PS Example 4; SEQ ID NO 9198; 650pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention

SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 479 AGTCCTGTTCTCTCCAC 496

Search completed: February 4, 2005, 21:52:42
Job time : 233.23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-5
Perfect score: 18
Sequence: 1 agctctgtctcttccac 18
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	279	2	AW247015
C 2	18	100.0	382	4	BM855440
C 3	18	100.0	395	4	BT030877
C 4	18	100.0	421	4	BM844286
C 5	18	100.0	421	6	CF145335
C 6	18	100.0	433	4	BT022254
C 7	18	100.0	474	7	CN422261
C 8	18	100.0	490	4	BG746308
C 9	18	100.0	503	1	AT283063
C 10	18	100.0	503	4	BM857244
C 11	18	100.0	542	7	CN422262
C 12	18	100.0	543	5	BX487587
C 13	18	100.0	560	6	CD675630
C 14	18	100.0	577	6	CF131978
C 15	18	100.0	584	1	AL134785
C 16	18	100.0	587	2	BE871836
C 17	18	100.0	596	2	AW732926
C 18	18	100.0	602	7	CN422268
C 19	18	100.0	616	2	BE783664
C 20	18	100.0	616	6	CF132307
C 21	18	100.0	619	2	BF038769
C 22	18	100.0	624	6	CF131456
C 23	18	100.0	632	7	CN422264
C 24	18	100.0	635	4	BI489889

C 25	18	100.0	657	2	BE207063
C 26	18	100.0	671	2	AW814739
C 27	18	100.0	688	4	BG708652
C 28	18	100.0	702	6	CF125275
C 29	18	100.0	704	4	BI561500
C 30	18	100.0	707	6	CD636467
C 31	18	100.0	711	2	BE535474
C 32	18	100.0	720	6	CD636470
C 33	18	100.0	726	2	BF116000
C 34	18	100.0	727	2	BE782921
C 35	18	100.0	731	4	BI766475
C 36	18	100.0	735	4	BI522819
C 37	18	100.0	735	6	CD641746
C 38	18	100.0	751	2	BE734566
C 39	18	100.0	776	2	BF529410
C 40	18	100.0	798	7	CK000319
C 41	18	100.0	821	5	BQ932013
C 42	18	100.0	830	7	CF619432
C 43	18	100.0	831	7	CO247250
C 44	18	100.0	834	4	BI550492
C 45	18	100.0	836	4	BM018295

ALIGNMENTS

RESULT 1
LOCUS AW247015/c
DEFINITION 2822471.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:282471 5', mRNA linear EST 07-JAN-2000
mRNA sequence.
ACCESSION AW247015
VERSION AW247015.1 GI:6590008
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 279)
NIT-MGC http://mgc.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
TITLE Unpublished (1999)
JOURNAL Other ESTs: 2822471.3prime
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project
Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Plate: LHCW9 row: H column: 24
High quality sequence stop: 199.
Location/Qualifiers
1. .279
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:282471"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
|||||
Db 161 AGTCCTGTTCTCTTCCAC 144

RESULT 2

BM855440/c
LOCUS BM855440 382 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0138319 S21SNU520 Homo sapiens cDNA clone S21SNU520-67-G02 5', mRNA sequence.

ACCESSION BM855440 GI:19211825
VERSION BM855440.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 382)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE

21C Frontier Korean EST Project 2001

JOURNAL

Unpublished (2002)

COMMENT

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 67 row: G column: 02
High quality sequence stop: 382.

FEATURES

source

1..382
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNU520-67-G02"
/sex="p"

/tissue_type="Stomach"
/cell_type="Floating aggregates"
/lab_host="Top10F"

/lab_host="Top10F"
/clone_lib="S21SNU520"
/notes="Organ: Stomach; Vector: pTZ18RPL; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTCCTGTTCTCTTCCAC 18
|||||
Db 341 AGTCCTGTTCTCTTCCAC 324

RESULT 3

BI030877/c
LOCUS BI030877 395 bp mRNA linear EST 14-JUN-2001
DEFINITION IL5-MT0262-290301-406-g10 MT0262 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI030877
VERSION BI030877.1 GI:14437507
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 395)
Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5&t2=IL5-MT0262-290301-406-g10&t3=2001-03-29&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 346.

FEATURES

source

1..395
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0262"

/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 395;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18
|||||
Db 369 AGTCCTGTTCTCTTCCAC 352

RESULT 4

BM844286/c
LOCUS BM844286 421 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0122378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5',


```

mRNA sequence.
ACCESSION   BM844286
VERSION     BM844286.1  GI:19200695
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 421)
AUTHORS    Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 63 row: B column: 03
            High quality sequence stop: 421.

FEATURES             Location/Qualifiers
     source           1..421
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S12SNU216-63-B03"
                     /sex="P"
                     /tissue_type="Lymph node"
                     /cell_type="Epithelial"
                     /lab_host="Top10P"
                     /clone_lib="S12SNU216"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN
Query Match      100.0%; Score 18; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  AGTCTGTTCTCTTCCAC 18
      |||||
Db   108 AGTCTGTTCTCTTCCAC 91

RESULT 5
LOCUS      CF145335/c
DEFINITION UI-HF-CBO-ash-f-06-0-UI.r1 NIH MGC_210 Homo sapiens cDNA clone
ACCESSION  CF145335
VERSION    CF145335.1  GI:33260779
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 421)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

mRNA sequence.
ACCESSION   BM844286
VERSION     BM844286.1  GI:19200695
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 421)
AUTHORS    Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 63 row: B column: 03
            High quality sequence stop: 421.

FEATURES             Location/Qualifiers
     source           1..421
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S12SNU216-63-B03"
                     /sex="P"
                     /tissue_type="Lymph node"
                     /cell_type="Epithelial"
                     /lab_host="Top10P"
                     /clone_lib="S12SNU216"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN
Query Match      100.0%; Score 18; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  AGTCTGTTCTCTTCCAC 18
      |||||
Db   108 AGTCTGTTCTCTTCCAC 91

RESULT 5
LOCUS      CF145335/c
DEFINITION UI-HF-CBO-ash-f-06-0-UI.r1 NIH MGC_210 Homo sapiens cDNA clone
ACCESSION  CF145335
VERSION    CF145335.1  GI:33260779
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 421)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 421)
AUTHORS    Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE      Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
PUBMED      8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Tim Ratliff
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/humanfl.html
            Seq primer: pYX-5.

FEATURES             Location/Qualifiers
     source           1..421
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30569057"
                     /tissue_type="CNCAP(3) T-225 cell line"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_MGC_210"
                     /note="Organ: Prostate; Vector: pT7T3 Pac; Site_1: EcoRI; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dt primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoRI adaptor, digested with Not I and then cloned directionally into pT7T3 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratliff."

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  AGTCTGTTCTCTTCCAC 18
      |||||
Db   102 AGTCTGTTCTCTTCCAC 85

RESULT 6
LOCUS      BI022254
DEFINITION CM3-MT0294-170101-631-c01 MT0294 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BI022254
VERSION    BI022254.1  GI:14428884
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 433)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

```

JOURNAL
MEDLINE
PUBMED
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICK Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM3&t2=CM3-MT0294-
170101-631-c01&t3=2001-01-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 433.

FEATURES
source
1..433
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0294"
/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 42 AGTCCTGTTCTCTCCAC 59
|||||

RESULT 7
CN422261/c
LOCUS
DEFINITION 17000424524125 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
ACCESSION CN422261
VERSION CN422261.1 GI:47409855
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murgue, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
TITLE Transcription characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 474 Std Error: 0.00.

FEATURES
source
1..474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/tissue type="embryonic stem cells, embryoid bodies
derived from HL, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="Oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from h9 cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN
Query Match 100.0%; Score 18; DB 7; Length 474;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 163 AGTCCTGTTCTCTCCAC 146
|||||

RESULT 8
BG746308/c
LOCUS
DEFINITION 602703549F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4856725 5',
mRNA sequence.
ACCESSION BG746308
VERSION BG746308.1 GI:14056961
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 490)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI708 row: a column: 14
High quality sequence stop: 464.

FEATURES
source
1..490
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4856725"
/tissue type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 15"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 242 AGTCCTGTTCTCTCCAC 225
|||||

RESULT 9
 AL283063 503 bp mRNA linear EST 29-JAN-1999
 LOCUS qm2c06.x1 Soares placenta 8to9weeks 2NBHP8to9w Homo sapiens CDNA
 DEFINITION clone IMAGE:1893322 3' similar to SW:BCIX_HUMAN Q07817 APOPTOSIS
 REGULATOR BCL-X. i, mRNA sequence.

ACCESSION AL283063
 VERSION AL283063.1 GI:3921296
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 503)
 REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1323 Std Error: 0.00
 Seq Primer: -40UP from Gibco
 High quality sequence stop: 440.

FEATURES
 source
 1. 503
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1893322"
 /dev_stage="two placentae: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: p7T3D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGAGCGCCGCAATTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p7T3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bernaldo."

ORIGIN
 Query Match 100.0%; Score 18; DB 1; Length 503;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTTCCAC 18
 |||||
 Db 458 AGTCCTGTTCTCTTCCAC 441

RESULT 10
 BM857244/c
 LOCUS K-EST0141477 S21SNU520 Homo sapiens CDNA clone S21SNU520-78-F09 5',
 DEFINITION mRNA sequence.
 ACCESSION BM857244
 VERSION BM857244.1 GI:19213643
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 503)
 REFERENCE Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)

COMMENT

Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 78 row: F column: 09
 High quality sequence stop: 503.
 Location/Qualifiers

FEATURES

source

1. 503
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S21SNU520-78-F09"
 /sex="F"
 /tissue_type="Stomach"
 /cell_type="floating aggregates"
 /cell_line="SNU-520"
 /lab_host="TOP10F"
 /clone_lib="S21SNU520"
 /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 503;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTTCCAC 18
 |||||
 Db 109 AGTCCTGTTCTCTTCCAC 92

RESULT 11

LOCUS

CN422262 542 bp mRNA linear EST 16-MAY-2004
 DEFINITION 17000424524143 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
 ACCESSION CN422262
 VERSION CN422262.1 GI:47409856
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 542)
 Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
 Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
 Lebkowski,J and Stanton,L.W.

TITLE

Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation

JOURNAL

COMMENT

Nat. Biotechnol. 22 (6), 707-716 (2004)
 Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com

```

Insert Length: 542   Std Error: 0.00.
Location/Qualifiers
1..542
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/notes="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from HES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN
Query Match      100.0%;   Score 18;   DB 7;   Length 542;
Best Local Similarity 100.0%;   Pred. No. 5.8e+02;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 171 AGTCCTGTTCTCTCCAC 154

RESULT 12
BX487587/c
LOCUS
DEFINITION
BX487587 543 bp mRNA linear EST 04-SEP-2003
DKFP686N10257_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFP686N10257 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 543)
Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Robo,G., Han,M. and Wiemann,S.
EST (Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-
Heine-University, Duesseldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No sl sequence available.
This clone (DKFP686N10257) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..543
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP686N10257"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/notes="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Query Match      100.0%;   Score 18;   DB 5;   Length 543;
Best Local Similarity 100.0%;   Pred. No. 5.8e+02;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 529 AGTCCTGTTCTCTCCAC 512

FEATURES
source
1..542
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP686N10257"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/notes="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Query Match      100.0%;   Score 18;   DB 6;   Length 560;
Best Local Similarity 100.0%;   Pred. No. 5.8e+02;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
|||||
Db 334 AGTCCTGTTCTCTCCAC 317

FEATURES
source
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fs25h07"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Lens cDNA (Normalized): fs"
/notes="Organ: Eye; Vector: pCMVSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(Cot 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Sequencing Center (NISC)."
```

```

RESULT 13
CD675630/c
LOCUS
DEFINITION
CD675630 560 bp mRNA linear EST 24-JUN-2003
fs25h07.y1 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone
fs25h07 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 560)
Wislow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,
Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human lens for the NEIBank
Project: over 2000 non-redundant transcripts, novel genes and
splice variants
Mol. Vis. 8 (4), 171-184 (2002)
22103463
12107413
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 25 row: h column: 07
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fs25h07"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Lens cDNA (Normalized): fs"
/notes="Organ: Eye; Vector: pCMVSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(Cot 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Sequencing Center (NISC)."
```

```

FEATURES
source
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fs25h07"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Lens cDNA (Normalized): fs"
/notes="Organ: Eye; Vector: pCMVSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(Cot 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Sequencing Center (NISC)."
```

```

RESULT 14
CF131978/c
LOCUS
DEFINITION
CF131978 577 bp mRNA linear EST 05-AUG-2003
UI-HF-FQ0-aws-e-16-0-UI.r1 NIH MGC_215 Homo sapiens cDNA clone
IMAGE:30553743 5', mRNA sequence.
ACCESSION
CF131978
```

```

VERSION      CF131978.1  GI:33214777
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 577)
AUTHORS      Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE        Normalization and subtraction: two approaches to facilitate gene
              discovery
JOURNAL      Genome Res. 6 (9), 791-806 (1996)
MEDLINE      97044477
PUBMED       889548
COMMENT      Contact: Soares, MB
              Coordinated Laboratory for Computational Genomics
              University of Iowa
              375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
              Tel: 319 335 8250
              Fax: 319 335 9565
              Email: bento-soares@uiowa.edu
              Tissue Procurement: Mary Hendrix
              cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
              cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: Distribution information can be found at
              http://genome.uiowa.edu/distribution/humanfl.html
              Seq primer: pYX-5.

FEATURES     source
              Location/Qualifiers
                1..577
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:30553743"
                /tissue_type="Chondrosarcoma Lung Metastasis cell lines"
                /lab_host="DH10B (T1 phage resistant)"
                /clone_lib="NIH_MGC_215"
                /note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
                Site 2: Not I; The library was constructed according
                Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                1996. Denatured RNA was size fractionated on a 1% agarose
                gel. First strand cDNA synthesis was primed with oligo-dT
                primer containing a Not I site. Double strand cDNA was
                size selected according to mRNA size fraction, ligated
                with EcoR I adaptor, digested with Not I and then cloned
                directionally into pYX-Asc vector. The library tag
                sequence located between the Not I site and the polyA tail
                is GATAAGGCCA. Tissue was provided by Mary Hendrix."

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 577;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGTCCTGTTCTCTTCCAC 18
        |||||
Db      248 AGTCCTGTTCTCTTCCAC 231

RESULT 15
AL134785/c
LOCUS       AL134785
DEFINITION DKF2p547K2090 r1 547 (synonym: hfb1) Homo sapiens cDNA clone
            DKF2p547K2090 5', mRNA sequence.
ACCESSION  AL134785
VERSION     AL134785.1  GI:6602972
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 584)
AUTHORS    Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
TITLE      EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and

```

```

Wiemann,S.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann. Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKF2p547K2090) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES     source
              Location/Qualifiers
                1..584
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="DKF2p547K2090"
                /tissue_type="brain"
                /dev_stage="fetal"
                /lab_host="Xi-2blue"
                /clone_lib="347 (synonym: hfb1)"
                /note="vector: pAMPI; Site 1: NotI; Site 2: SalI"

ORIGIN
Query Match      100.0%; Score 18; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGTCCTGTTCTCTTCCAC 18
        |||||
Db      138 AGTCCTGTTCTCTTCCAC 121

Search completed: February 5, 2005, 08:11:42
Job time : 2151.2 secs

```

JOURNAL
COMMENT

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39, Search time 432.664 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169a-6
Perfect score: 18
Sequence: 1 ctttactgctgcatggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644845745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenEmbl.*

- 1: gb_ba.*
- 2: gb_hug.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235154
2	18	100.0	18	6	BD235170
3	18	100.0	512	6	CQ727769
4	18	100.0	555	6	CQ113695
5	18	100.0	555	6	CQ152574
6	18	100.0	555	6	CQ185831
7	18	100.0	555	6	CQ235904
8	18	100.0	555	6	CQ273477
9	18	100.0	555	6	CQ310858
10	18	100.0	555	6	CQ347773
11	18	100.0	600	6	CQ100639
12	18	100.0	600	6	CQ139631
13	18	100.0	600	6	CQ175964
14	18	100.0	600	6	CQ222999
15	18	100.0	600	6	CQ260961
16	18	100.0	600	6	CQ298444
17	18	100.0	600	6	CQ335104
18	18	100.0	636	6	BD097037
19	18	100.0	702	6	BD084108

c 20	18	100.0	702	6	BD102202
c 21	18	100.0	702	9	BT007208
c 22	18	100.0	702	12	BT008248
c 23	18	100.0	723	9	HSU72398
c 24	18	100.0	737	6	AR054022
c 25	18	100.0	737	6	AR172595
c 26	18	100.0	737	6	IS2012
c 27	18	100.0	737	6	AR371662
c 28	18	100.0	737	6	AR380913
c 29	18	100.0	737	9	HSBCLXS
c 30	18	100.0	747	6	AX127722
c 31	18	100.0	926	6	AR054021
c 32	18	100.0	926	6	AR118504
c 33	18	100.0	926	6	AR124952
c 34	18	100.0	926	6	AR144311
c 35	18	100.0	926	6	AR172594
c 36	18	100.0	926	6	BD243042
c 37	18	100.0	926	6	CQ765842
c 38	18	100.0	926	6	ES8777
c 39	18	100.0	926	6	IS2011
c 40	18	100.0	926	6	AR371661
c 41	18	100.0	926	6	AR380885
c 42	18	100.0	926	6	AX839772
c 43	18	100.0	926	6	AX925686
c 44	18	100.0	926	9	HSBCLXL
c 45	18	100.0	1236	6	AX085490

ALIGNMENTS

RESULT 1
BD235154
LOCUS BD235154 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION BD235154
VERSION BD235154.1 GI:33044924
KEYWORDS JP 2002519048-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Stein, C.A.
TITLE Oligonucleotide inhibitors of bcl-xL
JOURNAL Patent: JP 2002519048-A 6 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT OS Artificial Sequence
PN JP 2002519048-A/6
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PI 02-JUL-1998 US 09/109614
CY A STEIN

PC C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC
A61K47/42,
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTACTGCTGCCATGGG 18
|||||||


```

VERSION      CQ152574.1  GI:41159924
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human bone marrow
JOURNAL      Patent: WO 0157276-A 22596 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     source
              1..555
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
                = 4.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
    |||||
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 6
CQ185831
LOCUS       CQ185831          555 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17227 from Patent WO0157274.
ACCESSION   CQ185831
VERSION     CQ185831.1  GI:41180846
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human heart
JOURNAL      Patent: WO 0157274-A 17227 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     source
              1..555
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
                1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN HIT:
                BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
    |||||
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 7
CQ235904
LOCUS       CQ235904          555 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 22743 from Patent WO0157273.
ACCESSION   CQ235904
VERSION     CQ235904.1  GI:41219182
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 21738 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     source
              1..555
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
                = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
    |||||
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 8
CQ273477
LOCUS       CQ273477          555 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21738 from Patent WO0157277.
ACCESSION   CQ273477
VERSION     CQ273477.1  GI:41246081
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 21738 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     source
              1..555
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
                = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
    |||||
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 9
CQ273477
LOCUS       CQ273477          555 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21738 from Patent WO0157277.
ACCESSION   CQ273477
VERSION     CQ273477.1  GI:41246081
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 21738 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     source
              1..555
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
                = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
    |||||
Db 304 CTTTACTGCTGCCATGGG 321

```

```
Db 304 CTTTACTGCTGCCATGGG 321
|||||
|||||

RESULT 9
CQ310858          555 bp DNA linear PAT 23-JAN-2004
LOCUS
DEFINITION Sequence 21963 from Patent WO0186003.
ACCESSION CQ310858
VERSION CQ310858.1 GI:41271435
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human lung
JOURNAL Patent: WO 0186003-A 21963 15-NOV-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
|||||

Db 304 CTTTACTGCTGCCATGGG 321
|||||
|||||

RESULT 10
CQ347773          555 bp DNA linear PAT 23-JAN-2004
LOCUS
DEFINITION Sequence 21867 from Patent WO0157275.
ACCESSION CQ347773
VERSION CQ347773.1 GI:41296844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 21867 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
|||||

Db 304 CTTTACTGCTGCCATGGG 321
|||||
|||||

RESULT 11
CQ100639          600 bp DNA linear PAT 21-JAN-2004
LOCUS
DEFINITION Sequence 9498 from Patent WO0157272.
ACCESSION CQ100639
VERSION CQ100639.1 GI:41069665
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 9498 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
|||||

Db 304 CTTTACTGCTGCCATGGG 321
|||||
|||||

RESULT 12
CQ139631          600 bp DNA linear PAT 21-JAN-2004
LOCUS
DEFINITION Sequence 9653 from Patent WO0157276.
ACCESSION CQ139631
VERSION CQ139631.1 GI:41097003
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 9653 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 4.7"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
|||||

Db 323 CTTTACTGCTGCCATGGG 340
|||||
|||||
```

RESULT 13
 CQ175964
 LOCUS Sequence 7360 from Patent WO0157274.
 DEFINITION
 ACCESSION CQ175964
 VERSION CQ175964.1 GI:41170703
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ANALYSIS OF GENE EXPRESSION IN HUMAN HEART
 PATENT: WO 0157274-A 7360 09-AUG-2001;
 Aecomica, Inc. (US)
 JOURNAL Location/Qualifiers
 FEATURES
 source
 1..600
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"

ORIGIN
 Query Match 100.0%; Score 18; DB 6; Length 600;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
 |||||
 Db 323 CTTTACTGCTGCCATGGG 340

RESULT 14
 CQ222999
 LOCUS Sequence 9838 from Patent WO0157273.
 DEFINITION
 ACCESSION CQ222999
 VERSION CQ222999.1 GI:41205280
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
 (03.10.00)<150> US 60/236,359<151> 27 September 2000
 (27.09.00)<150> US 60/234,687<151> 21 September 2000
 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
 Molecular Dynamics Sequence Listing Engine
 PATENT: WO 0157273-A 9838 09-AUG-2001;
 Aecomica, Inc. (US)
 JOURNAL Location/Qualifiers
 FEATURES
 source
 1..600
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
 = 1.7"

ORIGIN
 Query Match 100.0%; Score 18; DB 6; Length 600;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
 |||||
 Db 323 CTTTACTGCTGCCATGGG 340

RESULT 15
 CQ260961
 LOCUS Sequence 9222 from Patent WO0157277.
 DEFINITION
 ACCESSION CQ260961
 VERSION CQ260961.1 GI:41233441
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
 HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER
 PATENT: WO 0157277-A 9222 09-AUG-2001;
 Aecomica, Inc. (US)
 JOURNAL Location/Qualifiers
 FEATURES
 source
 1..600
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
 = 3.5"

ORIGIN
 Query Match 100.0%; Score 18; DB 6; Length 600;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
 |||||
 Db 323 CTTTACTGCTGCCATGGG 340

Search completed: February 4, 2005, 23:30:40
 Job time : 432.664 secs

THIS PAGE LEFT BLANK

The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
 CC represent antisense oligos specific for the bcl-Xl mRNA

XX Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
 |||||
 Db 1 CTTTACTGCTGCCATGGG 18

RESULT 2
 ABA73433
 ID ABA73433 standard; DNA; 555 BP.

XX AC ABA73433;
 XX DT 01-FEB-2002 (first entry)
 XX DE Human foetal liver single exon nucleic acid probe #21738.
 XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX OS Homo sapiens.
 XX PN WO200157277-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000669.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 gene expression in human fetal liver.
 XX Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
 |||||
 Db 304 CTTTACTGCTGCCATGGG 321

RESULT 3
 AAI53868
 ID AAI53868 standard; DNA; 555 BP.

XX AC AAI53868;
 XX DT 17-OCT-2001 (first entry)
 XX DE Probe #22554 used to measure gene expression in human placenta sample.
 XX KW Probe; microarray; human; placenta; antenatal diagnosis;
 XX KW genetic disorder; ss.

XX OS Homo sapiens.
 XX PN WO200157272-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000663.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 gene expression in human placenta.
 XX Claim 25; SEQ ID NO 22554; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders

SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
 |||||
 Db 304 CTTTACTGCTGCCATGGG 321

RESULT 4
 ABA38761
 ID ABA38761 standard; DNA; 555 BP.

XX AC ABA38761;
 XX DT 23-JAN-2002 (first entry)

XX DE Probe #17227 for gene expression analysis in human heart cell sample.
 XX KW Human; gene expression; heart; microarray; vascular system; probe;
 XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
 XX KW congenital heart disease; ss.

```
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-48899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
PT
XX
XX Claim 4; SEQ ID NO 17227; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 5
AAK48039
ID AAK48039 standard; DNA; 555 BP.
XX
XX AAK48039;
XX
XX 06-NOV-2001. (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 22596.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PR
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
PT
XX
```

```
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-48899/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
PT
XX
XX Example 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 6
AAK21876
ID AAK21876 standard; DNA; 555 BP.
XX
XX AAK21876;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 21867.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
PT
XX
```

```
XX
PS Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
CC
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321
RESULT 7
ABS47753
ID ABS47753 standard; DNA; 555 BP.
XX
AC ABS47753;
XX
XX 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID No 22743.
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-48898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 4; SEQ ID NO 22743; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (i) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABS25011-ABS51005 represent human
```

```
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321
RESULT 8
ABS21972
ID ABS21972 standard; DNA; 555 BP.
XX
AC ABS21972;
XX
XX 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 21963.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 4; SEQ ID NO 21963; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX ; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
```


mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberculous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pt_sequences

Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 9

ACH87595
ID ACH87595 standard; DNA; 564 BP.

XX ACH87595;

DT 29-JUL-2004 (first entry)

DE Human genome derived single exon probe #20790.

XX Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

XX (RANK/) RANK D R.

XX (HANK/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.

XX Claim 1; SEQ ID NO 20790; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above). The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030194704

XX Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 564;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18

Db 304 CTTTACTGCTGCCATGGG 321

RESULT 10

ABA60917

ID ABA60917 standard; DNA; 600 BP.

XX ABA60917;

DT 01-FEB-2002 (first entry)

XX Human foetal liver: single exon nucleic acid probe #9222.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

```

PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.
XX Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human fetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human fetal liver. The
XX present sequence is a single exon nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
DB 323 CTTTACTGCTGCCATGGG 340
RESULT 12
ID ABA28894
XX ABA28894 standard; DNA; 600 BP.
XX AC ABA28894;
XX XX
XX 23-JAN-2002 (first entry)
XX Probe #7360 for gene expression analysis in human heart cell sample.
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX Homo sapiens.
XX XX
XX WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488899/53.
XX DR Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX PT Claim 1; SEQ ID NO 7360; 530pp; English.
XX PS The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic

```

```

CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTTTACTGCTGCCATGGG 18
Db 323 CTTTACTGCTGCCATGGG 340

RESULT 13
AAK35096
ID AAK35096 standard; DNA; 600 BP.
XX
AC AAK35096;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTTTACTGCTGCCATGGG 18
Db 323 CTTTACTGCTGCCATGGG 340

RESULT 14
AAK09207

```

```

ID AAK09207 standard; DNA; 600 BP.
XX
AC AAK09207;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 9198.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
PS Example 4; SEQ ID NO 9198; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTTTACTGCTGCCATGGG 18
Db 323 CTTTACTGCTGCCATGGG 340

RESULT 15
ABS34848
ID ABS34848 standard; DNA; 600 BP.
XX
AC ABS34848;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID No 9838.
XX
KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
OS Homo sapiens.

```

XX WO200157273-A2.
PN
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488898/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
XX Claim 1; SEQ ID NO 9838; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||
Db 323 CTTTACTGCTGCCATGGG 340

Search completed: February 4, 2005, 21:52:42
Job time : 232.23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-6
Perfect score: 18
Sequence: 1 cttactgctgccatg99 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	244	2	BE818726
C 2	18	100.0	294	2	BE818722
C 3	18	100.0	310	4	BI060608
C 4	18	100.0	317	4	BI045645
C 5	18	100.0	344	8	AZ576742
C 6	18	100.0	421	4	BM844286
C 7	18	100.0	421	6	CF145335
C 8	18	100.0	456	8	AZ537061
C 9	18	100.0	474	7	CN422261
C 10	18	100.0	475	5	BQ331598
C 11	18	100.0	490	4	BG746308
C 12	18	100.0	503	4	BM857244
C 13	18	100.0	516	7	H09884
C 14	18	100.0	542	7	CN422262
C 15	18	100.0	560	6	CD675630
C 16	18	100.0	577	6	CF131978
C 17	18	100.0	584	1	AL134785
C 18	18	100.0	587	2	BE871836
C 19	18	100.0	596	2	AW732926
C 20	18	100.0	612	2	BE783664
C 21	18	100.0	619	2	BF038769
C 22	18	100.0	624	6	CF131456
C 23	18	100.0	632	7	CN422264
C 24	18	100.0	635	4	BI489889

C 25	18	100.0	648	4	BM011754
C 26	18	100.0	657	2	BE207063
C 27	18	100.0	671	2	AW814739
C 28	18	100.0	688	4	BG708652
C 29	18	100.0	697	4	BI457116
C 30	18	100.0	700	4	EG831301
C 31	18	100.0	704	4	BI561500
C 32	18	100.0	705	4	BG290422
C 33	18	100.0	711	6	CD636467
C 34	18	100.0	712	2	BE535474
C 35	18	100.0	720	6	CD636470
C 36	18	100.0	726	2	BF116000
C 37	18	100.0	731	4	BI766475
C 38	18	100.0	735	4	BI522819
C 39	18	100.0	735	6	CD641746
C 40	18	100.0	798	5	BQ687097
C 41	18	100.0	798	7	CK000319
C 42	18	100.0	818	4	EG824757
C 43	18	100.0	821	5	BQ932013
C 44	18	100.0	826	4	EG766191
C 45	18	100.0	830	7	CF619432

ALIGNMENTS

RESULT 1
BE818726/c
LOCUS BE818726 244 bp mRNA linear EST 21-SEP-2000
DEFINITION PM3-BN0300-180700-003-c06 BN0300 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE818726
VERSION BE818726.1 GI:10250960
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 244)
AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc.Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20204663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-pm3-BN0300-180700-003-c06&t3=2000-07-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 223.
Location/Qualifiers
1. 244
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0300"

FEATURES
source

note="Organ: breast normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
Db 59 CTTTACTGCTGCCATGGG 42

RESULT 2

BE818722/c
LOCUS 294 bp mRNA linear EST 21-SEP-2000
DEFINITION PM3-BN0300-080700-002-g11 BN0300 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE818722
VERSION BE818722.1 GI:10250956
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 294)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=PM3-BN0300-080700-002-g11&t3=2000-07-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 294.

FEATURES
source Location/Qualifiers
1..294
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0300"
/note="Organ: breast normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
Db 101 CTTTACTGCTGCCATGGG 84

RESULT 3

BI060608
LOCUS 310 bp mRNA linear EST 15-JUN-2001
DEFINITION IL3-UT0115-300101-433-B03 UT0115 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI060608
VERSION BI060608.1 GI:14468135
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 310)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL3&t2=IL3-UT0115-300101-433-B03&t3=2001-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 310.

FEATURES
source Location/Qualifiers
1..310
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0115"
/note="Organ: uterus tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
Db 183 CTTTACTGCTGCCATGGG 200

RESULT 4

BI045645
LOCUS 317 bp mRNA linear EST 14-JUN-2001
DEFINITION MR3-FN0206-300101-004-h07 FN0206 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI045645

VERSION B1045645.1 GI:14452267
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 317)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=WR3&t2=WR3-FN0206-300101-004-h07&t3=2001-01-30&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 11
 High quality sequence stop: 317.
FEATURES
 source
 1..317
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="FN0206"
 /note="Organ: prostate normal; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
 Query Match 100.0%; Score 18; DB 4; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CTTTACTGCTGCCATGGG 18
 |||||
 Db 110 CTTTACTGCTGCCATGGG 127
 |||||
RESULT 5
 A2576742 344 bp DNA linear GSS 06-DEC-2000
 LOCUS AST-2700919 Genetrap T47D Human Breast Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.
DEFINITION A2576742
VERSION A2576742.1 GI:11563053
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 344)
 Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M., Bernardino, A., Durick, K. and Pollok, B.

TITLE Exon-trap tags from a T47D GenomeScreen(TM) Library
JOURNAL Unpublished (2000)
COMMENT Contact: Greg Henkel
 Gene Expression
 Aurora Biosciences Corp.
 11010 Torreyana Road, San Diego, CA 92121, USA
 Tel: 8584048436
 Fax: 8584046719
 Email: henkel@aurabio.com
 Pools of cells were isolated from a Genomescreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase preceded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was cloned in pamp-1 and used to transform DHS-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.
 Class: exon-trapped.
FEATURES
 Location/Qualifiers
 1..344
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /tissue_type="Carcinoma"
 /cell_type="Epithelial"
 /cell_line="T47D"
 /clone_lib="Genetrap T47D Human Breast Carcinoma Library"
 /note="Organ: Breast; Vector: pamp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pamp-1 and used to transform DHS-alpha competent bacteria."
ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CTTTACTGCTGCCATGGG 18
 |||||
 Db 185 CTTTACTGCTGCCATGGG 202
 |||||
RESULT 6
 BM844286/c 421 bp mRNA linear EST 06-MAR-2002
 LOCUS K-EST0122378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5', mRNA sequence.
DEFINITION BM844286
ACCESSION BM844286
VERSION BM844286.1 GI:19200695
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 421)
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, H.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 21C Frontier Korean EST Project 2001
TITLE Unpublished (2002)
JOURNAL Contact: Kim YS
COMMENT Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongseung@mail.kribb.re.kr
 Plate: 63 row: B column: 03
 High quality sequence stop: 421.
FEATURES
 Location/Qualifiers
 1..421
 /organism="Homo sapiens"

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S128NU216-83-B03"
/sex="F"
/tissue_type="Lymph node"
/cell_type="Epithelial"
/cell_line="SNU-216"
/lab_host="TSP10P"
/clone_lib="S128NU216"
/notes="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10p by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
Db 264 CTTTACTGCTGCCATGGG 247

RESULT 7
CF145335/c
LOCUS CF145335 421 bp mRNA linear EST 06-AUG-2003
DEFINITION UI-HF-C80-asn-f-06-0-UI-r1 NIH_MGC_210 Homo sapiens cDNA clone IMAGE:30569057 5', mRNA sequence.
ACCESSION CF145335
VERSION CF145335.1 GI:33260779
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalizati on and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
CONTACT Soares, MB
Coordinated Laboratory for Computational Genomics
UNIVERSITY OF IOWA
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Tim Ratliff
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pYX-5.
Location/Qualifiers
1. .421
/mol_type="mRNA"
/organism="Homo sapiens"

FEATURES
source
1. .421
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="Epithelial"
/cell_type="Epithelial"
/cell_line="PC-3"
/clone_lib="Genetrap PC-3 Human Prostatic Carcinoma Library"
/notes="Organ: Prostate; Vector: pAmp-1; 3' RACE of total

/db_xref="taxon:9606"
/clone="IMAGE:30569057"
/tissue_type="CNCAP(3)T-225 cell line"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH MGC 210"
/notes="Organ: Prostate; Vector: pT7T3 Pac; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size sorted according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pT7T3 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratliff."

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
Db 258 CTTTACTGCTGCCATGGG 241

RESULT 8
AZ537061
LOCUS AZ537061 456 bp DNA linear GSS 06-NOV-2000
DEFINITION AST-2P01514.AB Genetrap PC-3 Human Prostatic Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.
ACCESSION AZ537061
VERSION AZ537061.1 GI:11113828
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M., Bernardino,A., Durick,K. and Pollok,B.
Exon-trap tags from a PC-3 GenomesScreen(TM) Library
Unpublished (2000)
CONTACT Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomesScreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase gene followed by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAMP-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.
Class: exon-trapped.
Location/Qualifiers
1. .456
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Adenocarcinoma"
/cell_type="Epithelial"
/cell_line="PC-3"
/clone_lib="Genetrap PC-3 Human Prostatic Carcinoma Library"
/notes="Organ: Prostate; Vector: pAmp-1; 3' RACE of total

```


RNA from genetrapp pools; shotgun clone in pAMP-1 and used to transform DH5-alpha competent bacteria."

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
|||||
Db 436 CTTTACTGCTGCCATGGG 453

RESULT 9

CN422261/c
LOCUS CN422261 474 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700424524125 GRN_EB Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN422261
VERSION CN422261.1 GI:47409855
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 474)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL

COMMENT Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760

Email: rbrandenberger@geron.com

Insert Length: 474 Std Error: 0.00.

FEATURES

Location/Qualifiers
1..474
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"

/clone_lib="GRN_EB"

/note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from HES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
|||||
Db 319 CTTTACTGCTGCCATGGG 302

RESULT 10

BQ331598/c
LOCUS BQ331598 475 bp mRNA linear EST 17-MAY-2002
DEFINITION MR4-ET0138-080501-010-406 ET0138 Homo sapiens cDNA, mRNA sequence.

ACCESSION BQ331598

VERSION BQ331598.1 GI:20972765

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 475)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

PUBMED

COMMENT

10737800
Contact: Simpson A.J.J.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ET0138-080501-010-406&t3=2001-05-08&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 41

High quality sequence stop: 475.

FEATURES

source

1..475
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev stage="Adult"

/clone_lib="ET0138"

/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;

Site2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (O.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
|||||
Db 153 CTTTACTGCTGCCATGGG 136

RESULT 11

BG746308/c
LOCUS BG746308 490 bp mRNA linear EST 15-MAY-2001
DEFINITION 602703549F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4856725 5', mRNA sequence.

ACCESSION BG746308

VERSION BG746308.1 GI:14056961

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 490)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: csapba-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1708 row: a column: 14
 High quality sequence stop: 464.

FEATURES

1. 490
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4856725"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_15"
 /notes="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 490;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18

Db 399 CTTTACTGCTGCCATGGG 382

RESULT 12

BM857244/c

LOCUS BM857244 503 bp mRNA linear EST 06-MAR-2002
 DEFINITION K-EST0141477 S21SNUS20 Homo sapiens cDNA clone S21SNUS20-78-F09 5',
 mRNA sequence.

ACCESSION BM857244

VERSION BM857244.1 GI:19213643

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 503)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongseung@mail.kribb.re.kr

Plate: 78 row: F column: 09

High quality sequence stop: 503.

Location/Qualifiers

1. 503

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S21SNUS20-78-F09"

/sex="F"

/tissue_type="Stomach"

/cell_type="Floating aggregates"

/cell_line="SNU-520"

/lab_host="Top10F"

/clone_lib="S21SNUS20"

/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F' by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 503;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18

Db 265 CTTTACTGCTGCCATGGG 248

RESULT 13

H09884/c

LOCUS

DEFINITION

H09884 516 bp mRNA linear EST 23-JUN-1995

YMO5b07.r1 Soares infant brain IN18 Homo sapiens cDNA clone

IMAGE:46778 5' similar to SP:A47537 A47537 APOPOSIS REGULATOR

BCL-X - ;, mRNA sequence.

ACCESSION H09884

VERSION H09884.1 GI:874706

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 516)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevasakis,S., Waterson,R., Williamson,A., Wohldmann,P. and
 Wilson,R.

THE WASHU-MERCK EST PROJECT

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

Insert Size: 1997

High quality sequence stops: 249

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1997 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 249.

Location/Qualifiers

1. 516

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:419319"

/db_xref="taxon:9606"

/clone="IMAGE:46778"

/sex="female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares infant brain IN18"

/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGGCGCCGACGAAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
|||||
Db 78 CTTTACTGCTGCCATGGG 61

RESULT 14

CN422262/c
LOCUS CN422262 542 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424524143 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN422262
VERSION CN422262.1 GI:47409856
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 542)

REFERENCE

AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.

TITLE

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL

COMMENT Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com

Insert Length: 542 Std Error: 0.00.

FEATURES

source

1..542
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dr primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
|||||
Db 327 CTTTACTGCTGCCATGGG 310

RESULT 15

CN422262/c
LOCUS CN422262 560 bp mRNA linear EST 24-JUN-2003
DEFINITION fs25h07.y1 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone

fs25h07 5', mRNA sequence.

CN422262/c

CD675630

EST. 1

KEYWORDS

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 560)

Wistow, G., Bernstein, S. L., Wyatt, M. K., Behal, A., Touchman, J. W.,

Bouffard, G., Smith, D. and Peterson, K.

Expressed sequence tag analysis of adult human lens for the NEtBank

Project: over 2000 non-redundant transcripts, novel genes and

splice variants

Mol. Vis. 8 (4), 171-184 (2002)

22103463

12107413

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 25 row: h column: 07

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

1..560

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="fs25h07"

/tissue_type="Adult"

/dev_stage="Adult"

/lab_host="EMDH10B"

/clone_lib="Human Lens cDNA (Normalized): fs"

/note="Organ: Eye; Vector: pCMVSPORT6; A human lens

library (by) was normalized by self-subtraction. One

portion of double stranded plasmid DNA representing the

library was linearized by NotI. This NotI digested library

was used as a template for biotinylated RNA synthesis

using SP6 RNA polymerase. Another portion of the double

stranded plasmid library was converted to single-stranded

circles in vitro using Gene II and Exonuclease III (Life

Technologies). Single-stranded DNA (1 mg) was hybridized

(Cot 500) with 41 mg of Bio-RNA and vector blocking

oligonucleotides. The hybridized Bio-RNA/ss-circles were

removed by streptavidin:phenol extraction. EST analysis

was performed on the library at the NIH Intramural

Sequencing Center(NISC)."

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
|||||
Db 490 CTTTACTGCTGCCATGGG 473

Search completed: February 5, 2005, 08:11:44
Job time : 2148.2 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 480.738 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-7
Perfect score: 20
Sequence: 1 cgcggtctctggtatccaa 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD235155
2	20	100.0	20	6	BD235171
3	20	100.0	541	4	AF245487
4	20	100.0	541	4	AF245488
5	20	100.0	541	4	AF245489
6	20	100.0	555	6	CQ113695
7	20	100.0	555	6	CQ113696
8	20	100.0	555	6	CQ113697
9	20	100.0	555	6	CQ113698
10	20	100.0	555	6	CQ113699
11	20	100.0	555	6	CQ113700
12	20	100.0	555	6	CQ113701
13	20	100.0	600	6	CQ113702
14	20	100.0	600	6	CQ113703
15	20	100.0	600	6	CQ113704
16	20	100.0	600	6	CQ113705
17	20	100.0	600	6	CQ113706
18	20	100.0	600	6	CQ113707
19	20	100.0	600	6	CQ113708

C 20	20	100.0	636	6	BD097037
C 21	20	100.0	695	6	AX525912
C 22	20	100.0	699	10	MMBCIXL
C 23	20	100.0	702	6	BD084108
C 24	20	100.0	702	6	BD102202
C 25	20	100.0	702	9	BT007208
C 26	20	100.0	702	10	MMU10101
C 27	20	100.0	702	12	BT008248
C 28	20	100.0	720	4	AF216205
C 29	20	100.0	723	9	HSU72398
C 30	20	100.0	726	10	RNU34963
C 31	20	100.0	726	10	S76513
C 32	20	100.0	747	6	AX127722
C 33	20	100.0	752	4	SSJ001203
C 34	20	100.0	764	10	RNU10579
C 35	20	100.0	765	4	AF164517
C 36	20	100.0	926	6	AR054021
C 37	20	100.0	926	6	AR118504
C 38	20	100.0	926	6	AR124952
C 39	20	100.0	926	6	AR144311
C 40	20	100.0	926	6	AR172594
C 41	20	100.0	926	6	BD243042
C 42	20	100.0	926	6	CQ765842
C 43	20	100.0	926	6	E58777
C 44	20	100.0	926	6	I52011
C 45	20	100.0	926	6	AR371661

ALIGNMENTS

RESULT 1
LOCUS BD235155 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xl.
ACCESSION BD235155
KEYWORDS BD235155.1 GI:33044925
SOURCE JP 2002519048-A/7.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Stein,C.A.
TITLE Oligonucleotide inhibitors of bcl-xl
JOURNAL Patent: JP 2002519048-A 7 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT OS Artificial Sequence
PN JP 2002519048-A/7
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PI 02-JUL-1998 US 09/109614
CY A STEIN

PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCGTTCCTCGATCCAA 20
|||||

Df	1	CGCCGTTCTCCTGGATCCAA	20
RESULT 2			
BD235171			
LOCUS	BD235171	20 bp	DNA
DEFINITION	Oligonucleotide inhibitors of bcl-xL.	linear	PAT 17-JUL-2003
ACCESSION	BD235171		
VERSION	BD235171.1	GI:33044941	
KEYWORDS	JP 2002519048-A/23.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Stein,C.A.		
TITLE	Oligonucleotide inhibitors of bcl-xL		
JOURNAL	Patent: JP 2002519048-A 23 02-JUL-2002;		
COMMENT	THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK		
	OS Artificial Sequence		
	PN JP 2002519048-A/23		
	PD 02-JUL-2002		
	PF 02-JUL-1999 JP 2000557839		
	PR 02-JUL-1998 US 09/109614		
	PI CY A STEIN		
	PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC A61K47/42,		
	CC A61K47/48, A61K48/00, A61P35/00, C12N15/00		
	CC ANTISENSE OLIGONUCLEOTIDE		
	CC PHOSPHOROTHIOATE LINKAGE		
	CC PHOSPHOROTHIOATE LINKAGE		
	CC PHOSPHOROTHIOATE LINKAGE		
	CC PHOSPHOROTHIOATE LINKAGE		
	CC PROPYNYL dC		
	CC PROPYNYL dC		
	CC PROPYNYL dC		
	CC PROPYNYL dC		
	CC PROPYNYL dT		
	CC PROPYNYL dT		
	CC PROPYNYL dT		
	CC PROPYNYL dT		
	CC PROPYNYL dT		
	FH Key	Location/Qualifiers	
	FT misc_binding	(1) . (2)	
	FT misc_binding	(3) . (5)	
	FT misc_binding	(6) . (12)	
	FT misc_binding	(17) . (20)	
	FT modified_base	(1) . (1)	
	FT modified_base	(3) . (4)	
	FT modified_base	(8) . (8)	
	FT modified_base	(10) . (11)	
	FT modified_base	(17) . (18)	
	FT modified_base	(6) . (7)	
	FT modified_base	(12) . (12)	
	FT modified_base	(16) . (16)	
	FT modified_base	(9) . (9)	
FEATURES	source	Location/Qualifiers	
	1. .20	/organism="synthetic construct"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:32630"	
ORIGIN			
Query Match	100.0%;	Score 20; DB 6; Length 20;	
Best Local Similarity	100.0%;	Pred. No. 8.5;	
Matches	20; Conservative	0; Mismatches	0; Indels
			0; Gaps
			0;
QY	1	CGCCGTTCTCCTGGATCCAA	20
Df	1	CGCCGTTCTCCTGGATCCAA	20
RESULT 3			

```

/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clones="1.2"
<i>..>541
/codon_start=1
/product="anti-apoptotic regulator Bcl-xL"
/protein_id="AAK31307.1"
/db_xref="GI:13591638"
/translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG
DEFELRRAPSDTSLQHIPTPGTAYQSFQVNVNELFRDGVNMGRIVAFFSFGGALCV
ESVDKQVLSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKGQERF
NRWELTGMTAGVVLGSLF"

ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||
Db 409 CGCGTTCTCTCGATCCAA 390

RESULT 5
AF245489/c
LOCUS      AF245489      541 bp      mRNA      linear      MAM 11-APR-2001
DEFINITION Bos taurus clone 1.3 anti-apoptotic regulator Bcl-xL mRNA, partial cds.
ACCESSION AF245489
VERSION AF245489.1 GI:13591639
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 541)
AUTHORS Amills,M. and Bouzat,J.
TITLE Characterization of the bovine bcl-xL gene and related pseudogenes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 541)
AUTHORS Amills,M. and Bouzat,J.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autònoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain
FEATURES
source
Location/Qualifiers
1..541
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clones="1.3"
<i>..>541
/codon_start=1
/product="anti-apoptotic regulator Bcl-xL"
/protein_id="AAK31308.1"
/db_xref="GI:13591640"
/translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG
DEFELRRAPSDTSLQHIPTPGTAYQSFQVNVNELFRDGVNMGRIVAFFSFGGALCV
ESVDKQVLSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKGQERF
NRWELTGMTAGVVLGSLF"

CDS
Query Match      100.0%; Score 20; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||
Db 409 CGCGTTCTCTCGATCCAA 390

ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||
Db 409 CGCGTTCTCTCGATCCAA 390

/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clones="1.2"
<i>..>541
/codon_start=1
/product="anti-apoptotic regulator Bcl-xL"
/protein_id="AAK31307.1"
/db_xref="GI:13591638"
/translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG
DEFELRRAPSDTSLQHIPTPGTAYQSFQVNVNELFRDGVNMGRIVAFFSFGGALCV
ESVDKQVLSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKGQERF
NRWELTGMTAGVVLGSLF"

ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||
Db 409 CGCGTTCTCTCGATCCAA 390

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/translation="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL = 0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST.HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE 0.00e+00"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||
Db 6 CGCGTTCTCTCGATCCAA 25

RESULT 6
CQ113695
LOCUS      CQ113695      555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 22554 from Patent WO0157272.
ACCESSION CQ113695
VERSION CQ113695.1 GI:41083565
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 22554 09-AUG-2001;
Aescmica, Inc. (US)
FEATURES
source
Location/Qualifiers
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/translation="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL = 0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST.HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE 0.00e+00"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||
Db 6 CGCGTTCTCTCGATCCAA 25

RESULT 7
CQ152574
LOCUS      CQ152574      555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 22596 from Patent WO0157276.
ACCESSION CQ152574
VERSION CQ152574.1 GI:41159924
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 22596 09-AUG-2001;
Aescmica, Inc. (US)
FEATURES
source
Location/Qualifiers
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/translation="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL = 4.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST.HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE 0.00e+00"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||
Db 6 CGCGTTCTCTCGATCCAA 25

```

```

RESULT 8
LOCUS      CQ185831
DEFINITION Sequence 17227 from Patent WO0157274.
ACCESSION  CQ185831
VERSION    CQ185831.1 GI:41180846
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human heart
JOURNAL   Patent: WO 0157274-A 17227 09-AUG-2001;
          Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
              1..555
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
              1.4-SWISSPROT HIT: Q07817, EVALUAE 1.00e-106-EST_HUMAN HIT:
              BE207063.1, EVALUAE 0.00e+00-NT HIT: U72398.1, EVALUAE
              0.00e+00"
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CGCCGTTCTCTCGATCCAA 20
    |||||
Db   6 CGCCGTTCTCTCGATCCAA 25

RESULT 9
LOCUS      CQ235904
DEFINITION Sequence 22743 from Patent WO0157273.
ACCESSION  CQ235904
VERSION    CQ235904.1 GI:41219182
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE     HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
          ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
          3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
          60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
          August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
          (03.10.00)<150> US 60/236,359<151> 27 September 2000
          (27.09.00)<150> US 60/234,687<151> 21 September 2000
          (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
          Molecular Dynamics Sequence Listing Engine
JOURNAL   Patent: WO 0157273-A 22743 09-AUG-2001;
          Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
              1..555
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
              = 1.7-SWISSPROT HIT: Q07817, EVALUAE 1.00e-106-EST_HUMAN
              HIT: BE207063.1, EVALUAE 0.00e+00-NT HIT: U72398.1, EVALUAE
              0.00e+00"
ORIGIN

```

```

Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CGCCGTTCTCTCGATCCAA 20
    |||||
Db   6 CGCCGTTCTCTCGATCCAA 25

RESULT 10
LOCUS      CQ273477
DEFINITION Sequence 21738 from Patent WO0157277.
ACCESSION  CQ273477
VERSION    CQ273477.1 GI:41246081
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human fetal liver
JOURNAL   Patent: WO 0157277-A 21738 09-AUG-2001;
          Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
              1..555
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
              = 3.5-SWISSPROT HIT: Q07817, EVALUAE 1.00e-106-EST_HUMAN
              HIT: BE207063.1, EVALUAE 0.00e+00-NT HIT: U72398.1, EVALUAE
              0.00e+00"
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CGCCGTTCTCTCGATCCAA 20
    |||||
Db   6 CGCCGTTCTCTCGATCCAA 25

RESULT 11
LOCUS      CQ310858
DEFINITION Sequence 21963 from Patent WO0186003.
ACCESSION  CQ310858
VERSION    CQ310858.1 GI:41271435
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human lung
JOURNAL   Patent: WO 0186003-A 21963 15-NOV-2001;
          Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
              1..555
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
              2-SWISSPROT HIT: Q07817, EVALUAE 1.00e-106-EST_HUMAN HIT:
              BE207063.1, EVALUAE 0.00e+00-NT HIT: U72398.1, EVALUAE
              0.00e+00"
ORIGIN

```


Query Match 100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20
|||||
Db 6 CGCGTTCTCTGGATCCAA 25

RESULT 12
LOCUS CQ347773 555 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21867 from Patent WO0157275.
ACCESSION CQ347773
VERSION CQ347773.1 GI:41296844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 21867 09-AUG-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20
|||||
Db 6 CGCGTTCTCTGGATCCAA 25

RESULT 13
LOCUS CQ100639 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 9498 from Patent WO0157272.
ACCESSION CQ100639
VERSION CQ100639.1 GI:41069665
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 9498 09-AUG-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source
1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20
|||||
Db 25 CGCGTTCTCTGGATCCAA 44

RESULT 14
LOCUS CQ139631 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 9653 from Patent WO0157276.
ACCESSION CQ139631
VERSION CQ139631.1 GI:41097003
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 9653 09-AUG-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source
1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 4.7"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20
|||||
Db 25 CGCGTTCTCTGGATCCAA 44

RESULT 15
LOCUS CQ175964 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 7360 from Patent WO0157274.
ACCESSION CQ175964
VERSION CQ175964.1 GI:41170703
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 7360 09-AUG-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source
1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCGTTCTCCTGGATCCAA 20
Dy 25 CGCCGTTCTCCTGGATCCAA 44

Search completed: February 4, 2005, 23:30:41
Job time : 481.738 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169A-7
Perfect score: 20
Sequence: 1 cgcgttctctggtaccca 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	Az46977 Bcl-Xl mr
2	20	100.0	337	10	Adk66037 Standardi
3	20	100.0	492	9	Ach46093 Human inf
4	20	100.0	555	4	Aba73433 Human foe
5	20	100.0	555	4	Aai53868 Probe #22
6	20	100.0	555	4	Aba38761 Probe #17
7	20	100.0	555	4	Aak48039 Human bon
8	20	100.0	555	4	Aak21876 Human bra
9	20	100.0	555	4	Abs47753 Human liv
10	20	100.0	555	6	Abs21972 Human gen
11	20	100.0	564	12	Ach87595 Human gen
12	20	100.0	600	4	Aba60917 Human foe
13	20	100.0	600	4	Aai40812 Probe #94
14	20	100.0	600	4	Aba28894 Probe #73
15	20	100.0	600	4	Aak35096 Human bon
16	20	100.0	600	4	Aak09207 Human bra
17	20	100.0	600	4	Abs34848 Human liv
18	20	100.0	600	4	Abs09558 Human liv
19	20	100.0	636	4	Aah48169 Mutant bc
20	20	100.0	695	6	Abt09346 Phase-1 R
21	20	100.0	702	5	Aah43464 cDNA clon

ALIGNMENTS

RESULT 1

Az46977
ID AAZ46977 standard; DNA; 20 BP.

XX AC AAZ46977;

XX DT 14-APR-2000 (first entry)

XX DE Bcl-Xl mRNA specific antisense oligo G.

XX KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;
XX KM lung; bladder; bcl-2; vascular lesion; antisense; ss.

XX OS Homo sapiens.

XX PN WC200001393-A2.

XX PD 13-JAN-2000.

XX PF 02-JUL-1999; 99WO-US015250.

XX PR 02-JUL-1998; 98US-00109614.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Stein CA;

XX DR WPI; 2000-137140/12.

XX PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

XX PS Claim 1; Fig 1; 69pp; English.

XX CC The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

Adm45994 Human apo
Adg65218 Human Bcl
Aaf30926 Human Bcl
Adg65209 Human Bcl
Aaq81698 Human thy
Aat40079 Bcl-XL ge
Aaz93614 Bcl-x gen
Aas15189 Human bcl
Aac90810 Human bcl
ABK84766 Human cDN
Abt16641 Human bcl
Add56779 Human bcl
Aad64187 Human bcl
Adi32104 Human cDN
Adh52630 Human ant
Ado19990 Human PRO
Adp13351 Renal cel
Aas00247 Bcl-XL-DT
Aav17638 Mouse BCL
Aas00250 LFN-Bcl-X
Ade85177 Farnesyl
Aaf75960 Rat wild-
Adb58615 Toxicity-
Adb53263 Primary r

c 22 20 100.0 702 12 ADM45994
c 23 20 100.0 739 12 ADG65218
c 24 20 100.0 747 4 AAF30926
c 25 20 100.0 747 12 ADG65209
c 26 20 100.0 926 2 AAQ81698
c 27 20 100.0 926 2 AAT40079
c 28 20 100.0 926 3 AAZ93614
c 29 20 100.0 926 4 AAS15189
c 30 20 100.0 926 4 AAC90810
c 31 20 100.0 926 6 ABK84766
c 32 20 100.0 926 8 ABT16641
c 33 20 100.0 926 10 ADD56779
c 34 20 100.0 926 10 AAD64187
c 35 20 100.0 926 11 ADI32104
c 36 20 100.0 926 12 ADH52630
c 37 20 100.0 926 12 ADO19990
c 38 20 100.0 926 12 ADP13351
c 39 20 100.0 1236 5 AAS00247
c 40 20 100.0 1384 2 AAV17638
c 41 20 100.0 1455 5 AAS00250
c 42 20 100.0 1466 10 ADE85177
c 43 20 100.0 1742 4 AAF75960
c 44 20 100.0 1748 10 ADB58615
c 45 20 100.0 1748 10 ADB53263

CC lesions. They can also be included with a carrier (and optionally tetra
CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
CC represent antisense oligos specific for the bcl-X1 mRNA
XX
SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGTTCTCTCGATCCAA 20
|||||
Db 1 CGCGGTTCTCTCGATCCAA 20

RESULT 2
ADK66037/c
ID ADK66037 standard; DNA; 337 BP.

XX AC ADK66037;

XX DT 06-MAY-2004 (first entry)

XX DE Standardized polynucleotide system polynucleotide #8.

XX ss; standardized polynucleotide system; medical diagnosis;
KW functional genomics; sample analysis; pharmacogenomics; sample analysis.
XX OS Unidentified.

XX PN DE10209071-Al.

XX PD 25-SEP-2003.

XX PF 28-FEB-2002; 2002DB-01009071.

XX PR 28-FEB-2002; 2002DB-01009071.

XX PA (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.

XX PI Koehler T, Rost A;

XX DR WPI; 2003-732912/70.

XX Standardized polynucleotide system, useful for quantitative, real-time
PT determination of nucleic acid, comprises stabilized standards, primers
PT and probe.

XX Claim 1; Page 7; 38pp; German.

XX The present invention relates to a standardized polynucleotide system,
CC which comprises at least one carrier nucleic acid, at least 3
CC oligonucleotides, as primers and target-specific, fluorescently labeled
CC probe and optionally at least one set of stabilized controls (standard
CC RNA or DNA) of known concentration and instructions. The system comprises
CC any of 20 sets of one control, two primers and one target-specific probe.
CC The standardized polynucleotide system can be used for quantitative, real
CC -time detection of target nucleic acids, especially analysis of genes or
CC gene products, e.g. for individualized medical diagnosis, in veterinary
CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,
CC pharmaceutical testing, analysis of food or environmental samples and
CC also for ultra-sensitive detection of proteins by immuno-PCR. The present
CC sequence is a polynucleotide used in the system of the invention.

XX SQ Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 337;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGTTCTCTCGATCCAA 20
|||||

Db 156 CGCGGTTCTCTCGATCCAA 137

RESULT 3
ACH46093/c

XX ID ACH46093 standard; cDNA; 492 BP.

XX AC ACH46093;

XX DT 13-OCT-2003 (first entry)

XX DE Human infant brain cDNA #156.

XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.

XX OS Homo sapiens.

XX PN US2003073623-Al.

XX PD 17-APR-2003.

XX PF 30-JUL-2001; 2001US-00918995.

XX PR 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.

XX (LABA/) LABAT I.

XX (STAC/) STACHE-CRAIN B.

XX (DICK/) DICKSON M C.

XX (JONE/) JONES L W.

XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.

XX Claim 1; SEQ ID NO 33305; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623

XX SQ Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 492;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGTTCTCTCGATCCAA 20
|||||

Db 340 CGCGGTTCTCTCGATCCAA 321

RESULT 4

ABA73433
ID ABA73433 standard; DNA; 555 BP.
XX
XX AC
XX ABA73433;
XX
XX
DT 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #21738.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200157277-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000669.
PF
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 30-JUN-2000; 2000US-00608408.
PR
XX 03-AUG-2000; 2000US-00632366.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX
XX WPI; 2001-483447/52.
DR
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
PT
XX
XX Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.
PS
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CGCGTTCCTCTGGATCAA 20
DB ||||||||||||||||
6 CGCGTTCCTCTGGATCAA 25

RESULT 5
AAI53868
ID AAI53868 standard; DNA; 555 BP.
XX
XX AC
XX AAI53868;
XX
XX
DT 17-OCT-2001 (first entry)
XX
XX Probe #22554 used to measure gene expression in human placenta sample.
DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
XX Homo sapiens.
OS
XX

QY 1 CGCGTTCTCTGGATCCAA 20
 DB 6 CGCGTTCTCTGGATCCAA 25

RESULT 9

ABS47753
 ID ABS47753 standard; DNA; 555 BP.

XX AC ABS47753;
 XX 25-FEB-2003 (first entry)
 XX Human liver single exon probe, SEQ ID No 22743.

XX Human; single exon nucleic acid probe; liver; cirrhosis;
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 KW coronary heart disease; ss.

XX Homo sapiens.

XX WO200157273-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000664.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.

XX Claim 4; SEQ ID NO 22743; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABS25011-ABS1005 represent human
 CC liver single exon nucleic acid probes of the invention. Note: The
 CC sequence information for this patent does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 555;

Best Local Similarity 100.0%; Pred. No. 9.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGTTCTCTGGATCCAA 20

DB 6 CGCGTTCTCTGGATCCAA 25

RESULT 10

ABS21972

ID ABS21972 standard; DNA; 555 BP.

XX AC ABS21972;

XX 19-AUG-2002 (first entry)

XX Human genome-derived single exon probe ORF from lung SEQ ID No 21963.

XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;

XX chronic obstructive pulmonary disease; interstitial lung disease;

XX familial idiopathic pulmonary fibrosis; neurofibromatosis;

XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;

XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

XX primary ciliary dyskinesia; pulmonary hypertension;

XX hyaline membrane disease; open reading frame; ORF.

XX Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US000665.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.

XX Claim 4; SEQ ID NO 21963; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC ; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung

CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a single exon probe open reading frame of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 555;

Best Local Similarity 100.0%; Pred. No. 9.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20

DB 6 CGCCGTTCTCTCGATCCAA 25

RESULT 11

ACH87595

ID ACH87595 standard; DNA; 564 BP.

XX ACH87595;

AC ACH87595;

DT 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #20790.

DE Human; probe; ss; gene expression; single exon probe; microarray;

XX alternative splicing event; genomic alteration.

KW Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

PI WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX Claim 1; SEQ ID NO 20790; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene

CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridizes under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX
 SQ Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 564;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20

DB 6 CGCCGTTCTCTCGATCCAA 25

RESULT 12

ABA60917

ID ABA60917 standard; DNA; 600 BP.

XX ABA60917;

AC ABA60917;

DT 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #9222.

DE Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

OS WO200157277-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human fetal liver.

XX Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.

Best Local Similarity 100.0%; PRed. NO. 9.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAK35096
ID AAK35096 standard; DNA; 600 BP.

AC AAK35096;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GE-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGTTCTCTGGATCCAA 20
DB 25 CGCGGTTCTCTGGATCCAA 44

Search completed: February 4, 2005, 21:52:42
Job time : 258.033 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-7
Perfect score: 20
Sequence: 1 cgccgttctctgatccaa 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	101	9	CL569679
C 2	20	100.0	107	9	CL569678
C 3	20	100.0	119	9	CL569637
C 4	20	100.0	119	9	CL569651
C 5	20	100.0	119	9	CL569677
C 6	20	100.0	119	9	CL569687
C 7	20	100.0	119	9	CL569770
C 8	20	100.0	119	9	CL569771
C 9	20	100.0	119	9	CL569805
C 10	20	100.0	119	9	CL569908
C 11	20	100.0	119	9	CL569911
C 12	20	100.0	119	9	CL570137
C 13	20	100.0	119	9	CL570142
C 14	20	100.0	125	9	CL569466
C 15	20	100.0	126	9	CL569669
C 16	20	100.0	126	9	CL569866
C 17	20	100.0	126	9	CL569869
C 18	20	100.0	126	9	CL569905
C 19	20	100.0	126	9	CL569975
C 20	20	100.0	126	9	CL569987
C 21	20	100.0	126	9	CL570033
C 22	20	100.0	127	9	CL569665
C 23	20	100.0	127	9	CL569672
C 24	20	100.0	127	9	CL569673

C 25	20	100.0	129	9	CL569909
C 26	20	100.0	132	9	CL569680
C 27	20	100.0	135	9	CL570034
C 28	20	100.0	165	9	CL569907
C 29	20	100.0	198	9	CL569873
C 30	20	100.0	201	9	CL569868
C 31	20	100.0	207	9	CL569540
C 32	20	100.0	211	9	CL569804
C 33	20	100.0	212	9	CL569870
C 34	20	100.0	212	9	CL569904
C 35	20	100.0	216	2	BF806802
C 36	20	100.0	231	4	BM818607
C 37	20	100.0	232	2	BF804861
C 38	20	100.0	251	9	CL569871
C 39	20	100.0	280	9	CL569872
C 40	20	100.0	283	2	BF823588
C 41	20	100.0	298	9	CL569565
C 42	20	100.0	299	7	F08773
C 43	20	100.0	305	4	BI399503
C 44	20	100.0	332	2	AW820481
C 45	20	100.0	356	2	AW244806

ALIGNMENTS

RESULT 1
CL569679/c
LOCUS
DEFINITION
A00730 Sanger Institute Gene Trap Library pGT01xr Mus musculus
CDNA, mRNA sequence.

ACCESSION
CL569679

VERSION
CL569679.2 GI:48774271

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

REFERENCE
Sanger Institute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48375778.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk

TITLE

JOURNAL

COMMENT

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES
source

Location/Qualifiers
1..101
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 101;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 20; Conservative 0; Mismatches 0; Gaps 0;

Oy 1 CGCGTTCTCTCTGGATCCAA 20

Db 91 CGCGTTCTCTCTGGATCCAA 72


```

ACCESSION   CL569677
VERSION     CL569677.2  GI:48774269
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 119)
AUTHORS     Sanger Institute Gene Trap Resource - SIGTR.
TITLE       http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL     Unpublished (2003)
COMMENT     On Jun 16, 2004 this sequence version replaced gi:48375776.
            Contact: Sanger Institute Gene Trap Resource - SIGTR
            Wellcome Trust Sanger Institute
            Email: info.genetrap@sanger.ac.uk
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from Sanger Institute Gene Trap
            Resource. Annotation information available from
            http://www.sanger.ac.uk/PostGenomics/genetrap/
            Class: Gene Trap.
            Location/Qualifiers
              1..119
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="129 OLA"
               /db_xref="taxon:10090"
               /sex="Male"
               /cell_type="Embryonic Stem Cell"
               /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
               /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||||
Db 114 CGCGTTCTCTCGATCCAA 95

RESULT 6
LOCUS       CL569687/c
DEFINITION  A00790 Sanger Institute Gene Trap Library pGT01xr Mus musculus
            cDNA, mRNA sequence.
ACCESSION   CL569687
VERSION     CL569687.2  GI:48774279
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 119)
AUTHORS     Sanger Institute Gene Trap Resource - SIGTR.
TITLE       http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL     Unpublished (2003)
COMMENT     On Jun 16, 2004 this sequence version replaced gi:48375786.
            Contact: Sanger Institute Gene Trap Resource - SIGTR
            Wellcome Trust Sanger Institute
            Email: info.genetrap@sanger.ac.uk
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from Sanger Institute Gene Trap
            Resource. Annotation information available from
            http://www.sanger.ac.uk/PostGenomics/genetrap/
            Class: Gene Trap.
            Location/Qualifiers
              1..119
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="129 OLA"

FEATURES             source
LOCUS       CL569687/c
DEFINITION  A00790 Sanger Institute Gene Trap Library pGT01xr Mus musculus
            cDNA, mRNA sequence.
ACCESSION   CL569687
VERSION     CL569687.2  GI:48774279
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 119)
AUTHORS     Sanger Institute Gene Trap Resource - SIGTR.
TITLE       http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL     Unpublished (2003)
COMMENT     On Jun 16, 2004 this sequence version replaced gi:48375869.
            Contact: Sanger Institute Gene Trap Resource - SIGTR
            Wellcome Trust Sanger Institute
            Email: info.genetrap@sanger.ac.uk
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from Sanger Institute Gene Trap
            Resource. Annotation information available from
            http://www.sanger.ac.uk/PostGenomics/genetrap/
            Class: Gene Trap.
            Location/Qualifiers
              1..119
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="129 OLA"
               /db_xref="taxon:10090"
               /sex="Male"
               /cell_type="Embryonic Stem Cell"
               /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
               /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||||
Db 114 CGCGTTCTCTCGATCCAA 95

RESULT 7
LOCUS       CL569770/c
DEFINITION  AR0256 Sanger Institute Gene Trap Library pGT01xr Mus musculus
            cDNA, mRNA sequence.
ACCESSION   CL569770
VERSION     CL569770.2  GI:48774362
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 119)
AUTHORS     Sanger Institute Gene Trap Resource - SIGTR.
TITLE       http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL     Unpublished (2003)
COMMENT     On Jun 16, 2004 this sequence version replaced gi:48375869.
            Contact: Sanger Institute Gene Trap Resource - SIGTR
            Wellcome Trust Sanger Institute
            Email: info.genetrap@sanger.ac.uk
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from Sanger Institute Gene Trap
            Resource. Annotation information available from
            http://www.sanger.ac.uk/PostGenomics/genetrap/
            Class: Gene Trap.
            Location/Qualifiers
              1..119
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="129 OLA"
               /db_xref="taxon:10090"
               /sex="Male"
               /cell_type="Embryonic Stem Cell"
               /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
               /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20
    |||||
Db 114 CGCGTTCTCTCGATCCAA 95

RESULT 8
LOCUS       CL569771/c
DEFINITION  AR0269 Sanger Institute Gene Trap Library pGT01xr Mus musculus
            cDNA, mRNA sequence.
ACCESSION   CL569771
VERSION     CL569771.2  GI:48774363
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 119)
Sanger Institute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48375870.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES
source
1. .119
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
|||||
Db 114 CGCCGTTCTCTCGATCCAA 95

RESULT 9
CL569805/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CL569805 119 bp mRNA linear GSS 16-JUN-2004
AR0493 Sanger Institute Gene Trap Library pGT01xr Mus musculus
cDNA, mRNA sequence.
CL569805
GSS.
CL569805.2 GI:48774397
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 119)
Sanger Institute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48375904.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES
source
1. .119
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
|||||
Db 114 CGCCGTTCTCTCGATCCAA 95

RESULT 10
CL569908/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CL569908 119 bp mRNA linear GSS 16-JUN-2004
AR1185 Sanger Institute Gene Trap Library pGT01xr Mus musculus
cDNA, mRNA sequence.
CL569908
GSS.
CL569908.2 GI:48774500
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 119)
Sanger Institute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48376007.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES
source
1. .119
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
|||||
Db 114 CGCCGTTCTCTCGATCCAA 95

RESULT 11
CL569911/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CL569911 119 bp mRNA linear GSS 16-JUN-2004
AR1189 Sanger Institute Gene Trap Library pGT01xr Mus musculus
cDNA, mRNA sequence.
CL569911
GSS.
CL569911.2 GI:48774503
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 119)
Sanger Institute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/

FEATURES
source
1. .119
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48376010.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetraps@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from <http://www.sanger.ac.uk/PostGenomics/genetraps/>
Class: Gene Trap.

FEATURES
source
Location/Qualifiers
1..119
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20
|||||
Db 114 CGCGTTCTCTGGATCCAA 95

RESULT 12
CL570137/c
LOCUS
DEFINITION AV0131 Sanger Institute Gene Trap Library pGT01xr Mus musculus
CDNA, mRNA sequence.
ACCESSION CL570137
VERSION CL570137.2 GI:48774729
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 119)
AUTHORS Sanger Institute Gene Trap Resource - SIGTR.
TITLE <http://www.sanger.ac.uk/PostGenomics/genetraps/>
JOURNAL Unpublished (2003)
COMMENT On Jun 16, 2004 this sequence version replaced gi:48376236.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetraps@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from <http://www.sanger.ac.uk/PostGenomics/genetraps/>
Class: Gene Trap.

FEATURES
source
Location/Qualifiers
1..119
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20
|||||
Db 114 CGCGTTCTCTGGATCCAA 95

Qy 1 CGCGTTCTCTGGATCCAA 20
|||||
Db 114 CGCGTTCTCTGGATCCAA 95

RESULT 13
CL570142/c
LOCUS
DEFINITION AV0189 Sanger Institute Gene Trap Library pGT01xr Mus musculus
CDNA, mRNA sequence.
ACCESSION CL570142
VERSION CL570142.2 GI:48774734
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 119)
AUTHORS Sanger Institute Gene Trap Resource - SIGTR.
TITLE <http://www.sanger.ac.uk/PostGenomics/genetraps/>
JOURNAL Unpublished (2003)
COMMENT On Jun 16, 2004 this sequence version replaced gi:48376241.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetraps@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from <http://www.sanger.ac.uk/PostGenomics/genetraps/>
Class: Gene Trap.

FEATURES
source
Location/Qualifiers
1..119
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20
|||||
Db 114 CGCGTTCTCTGGATCCAA 95

RESULT 14
CL569466/c
LOCUS
DEFINITION AN0071 Sanger Institute Gene Trap Library pGT01xr Mus musculus
CDNA, mRNA sequence.
ACCESSION CL569466
VERSION CL569466.2 GI:48774058
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 125)
AUTHORS Sanger Institute Gene Trap Resource - SIGTR.
TITLE <http://www.sanger.ac.uk/PostGenomics/genetraps/>
JOURNAL Unpublished (2003)
COMMENT On Jun 16, 2004 this sequence version replaced gi:48375565.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetraps@sanger.ac.uk

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from <http://www.sanger.ac.uk/PostGenomics/genetrp/>
Class: Gene Trap.

FEATURES
source

1..125
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 125;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTGGATCCAA 20
|||||
Db 120 CGCCGTTCTCTGGATCCAA 101

RESULT 15
CL569669/c

LOCUS CL569669 126 bp mRNA linear GSS 16-JUN-2004
DEFINITION AQ0663 Sanger Institute Gene Trap Library pGT01xr Mus musculus
CDNA, mRNA sequence.
ACCESSION CL569669
VERSION CL569669.2 GI:48774261
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 126)
Sanger Institute Gene Trap Resource - SIGTR.
TITLE <http://www.sanger.ac.uk/PostGenomics/genetrp/>
JOURNAL Unpublished (2003)
COMMENT On Jun 16, 2004 this sequence version replaced gi:48375768.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrp@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from <http://www.sanger.ac.uk/PostGenomics/genetrp/>
Class: Gene Trap.

FEATURES
source

1..126
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 126;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTGGATCCAA 20
|||||
Db 121 CGCCGTTCTCTGGATCCAA 102

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-8
Perfect score: 18
Sequence: 1 ctgactccagctgtatcc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235156
2	18	100.0	18	6	BD235173
3	18	100.0	18	6	BD235174
C 4	18	100.0	65	6	CQ559048
C 5	18	100.0	512	6	CQ727769
C 6	18	100.0	513	10	MMU10100
C 7	18	100.0	513	10	AF136230
C 8	18	100.0	513	10	AF279286
C 9	18	100.0	537	10	S78284
10	18	100.0	555	6	CQ113695
11	18	100.0	555	6	CQ152574
12	18	100.0	555	6	CQ185831
13	18	100.0	555	6	CQ235904
14	18	100.0	555	6	CQ273477
15	18	100.0	555	6	CQ310858
16	18	100.0	555	6	CQ347773
17	18	100.0	600	6	CQ106639
18	18	100.0	600	6	CQ139631
19	18	100.0	600	6	CQ175964

20	18	100.0	600	6	CQ222999
21	18	100.0	600	6	CQ260961
22	18	100.0	600	6	CQ298444
23	18	100.0	600	6	CQ335104
C 24	18	100.0	600	6	AX925692
C 25	18	100.0	660	6	AX925694
C 26	18	100.0	660	6	AX925696
C 27	18	100.0	695	6	AX525912
C 28	18	100.0	699	10	MMBCXLX
C 29	18	100.0	702	4	AY005131
C 30	18	100.0	702	6	BD084108
C 31	18	100.0	702	6	BD102202
C 32	18	100.0	702	9	BT007208
C 33	18	100.0	702	10	MMU10101
C 34	18	100.0	702	12	BT008248
C 35	18	100.0	720	4	AF216205
C 36	18	100.0	723	9	HSU72398
C 37	18	100.0	726	10	RNU34963
C 38	18	100.0	726	10	S76513
C 39	18	100.0	737	6	AR054022
C 40	18	100.0	737	6	AR172595
C 41	18	100.0	737	6	I52012
C 42	18	100.0	737	6	AR371662
C 43	18	100.0	737	6	AR380913
C 44	18	100.0	737	9	HSBCLXS
C 45	18	100.0	747	6	AX127722

ALIGNMENTS

RESULT 1
LOCUS BD235156 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xl.
ACCESSION BD235156
VERSION BD235156.1 GI:33044926
KEYWORDS JP 2002519048-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Stein,C.A.
TITLE Oligonucleotide inhibitors of bcl-xl
JOURNAL Patent: JP 2002519048-A 8 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT OS Artificial Sequence
PN JP 2002519048-A/8
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PI 02-JUL-1998 US 09/109614
CY A STEIN

PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence',
source Location/Qualifiers
1..18
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACTCCAGCTGTATCC 18
|||||

```
Db      1  CTGACTCCAGCTGTATCC 18

RESULT 2
BD235173
LOCUS      BD235173
DEFINITION Oligonucleotide inhibitors of bcl-xL
ACCESSION  BD235173
VERSION    BD235173.1 GI:33044943
KEYWORDS   JP 2002519048-A/25.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Stein, C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 25 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/25
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC

C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC
A61K47/42,
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
FH Key Location/Qualifiers
FT misc_binding (1)..(4)
FT propynyl dc
FT propynyl dt
FT propynyl dc
FT propynyl dt
FT propynyl dt
FT propynyl dt
FT propynyl dt
FT propynyl dt
FT propynyl dc
FT misc_binding (5)..(8)
FT misc_binding (11)..(12)
FT misc_binding (15)..(18)
FT modified_base (1)..(1)
FT modified_base (2)..(2)
FT modified_base (5)..(5)
FT modified_base (6)..(6)
FT modified_base (7)..(8)
FT modified_base (11)..(11)
FT modified_base (12)..(12)
FT modified_base (14)..(14)
FT modified_base (16)..(16)
FT modified_base (17)..(17).
FEATURES             Location/Qualifiers
     source           1..18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CTGACTCCAGCTGTATCC 18
        |||||
DB      1  CTGACTCCAGCTGTATCC 18

RESULT 4
CQ559048/c
LOCUS      CQ559048
DEFINITION Sequence 28683 from Patent WO0210449.
ACCESSION  CQ559048
VERSION    CQ559048.1 GI:41525475
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1
AUTHORS    Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE      Oligonucleotide library for detecting rna transcripts and splice
           variants that populate a transcriptome
JOURNAL    Patent: WO 0210449-A 28683 07-FEB-2002;
           Compugen Inc. (US)
FEATURES             Location/Qualifiers
     source           1..65
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"

Db      1  CTGACTCCAGCTGTATCC 18
```

/db_xref="taxon:10090"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 65;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
 |||||
 Db 31 CTGACTCCAGCTGTATCC 14

RESULT 5

LOCUS CQ727769/c 512 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 13703 from Patent WO02068579.
 ACCESSION CQ727769
 VERSION CQ727769.1 GI:42294740

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 Kits, such as nucleic acid arrays, comprising a majority of
 human exons or transcripts, for detecting expression and other uses
 thereof

JOURNAL Patent: WO 02068579-A 13703 06-SEP-2002;
 PE Corporation (NY) (US)

FEATURES
 source

1. 512
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 512;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
 |||||
 Db 212 CTGACTCCAGCTGTATCC 195

RESULT 6

LOCUS MMU10100/c 513 bp mRNA linear ROD 30-NOV-1995
 DEFINITION Mus musculus bcl-x short (bcl-x long) mRNA, complete cds.
 ACCESSION U10100
 VERSION U10100.1 GI:506645

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 513)
 Fang, W., Rivard, J.J., Mueller, D.L. and Behrens, T.W.

AUTHORS

T Cloning and molecular characterization of mouse bcl-x in B and T
 lymphocytes

JOURNAL

J. Immunol. 153 (10), 4388-4398 (1994)

MEDLINE

95052604

PUBMED

7963517

REFERENCE

2 (bases 1 to 513)
 Behrens, T.W.

AUTHORS

Submitted (26-MAY-1994) Timothy W. Behrens, Medicine, University of
 Minnesota, 515 Delaware St. S.E., Minneapolis, MN 55455, USA

JOURNAL

Location/Qualifiers

FEATURES

1. 513
 /organism="Mus musculus"
 /mol_type="mRNA"

RESULT 8

/db_xref="taxon:10090"
 /cell_line="WEHI 265.1 RNA"
 /note="alternatively spliced transcript of bcl-x long,
 GenBank Accession Number U10101"

gene
 CDS

1. 513
 /genes="bcl-x long"
 1. 513
 /gene="bcl-x long"
 /codon_start=1
 /product="bcl-x short"
 /protein_id="AAA82172.1"
 /db_xref="GI:506646"
 /translation="MQSNRELVVDFLSVKLSQKYSWSQFSQVDEENRTEAPEETEAE
 RETPSAINGNPWSHLADSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEFLRYR
 RAPSDTSQLHITPGTAYQSFQDTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGV
 VLLGSLFSRK"

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 513;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
 |||||
 Db 78 CTGACTCCAGCTGTATCC 61

RESULT 7

LOCUS AF136230/c 513 bp mRNA linear ROD 01-JUN-1999
 DEFINITION Rattus norvegicus bcl-x short mRNA, complete cds.
 ACCESSION AF136230
 VERSION AF136230.1 GI:4928687

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

1 (bases 1 to 513)
 He, X.J., Jin, K.L., Graham, S.H. and Simon, R.P.

AUTHORS

Direct Submission

TITLE

Submitted (22-MAR-1999) Neurology, University of Pittsburgh, 3500
 Terrace Street, Pittsburgh, PA 15213, USA

JOURNAL

Location/Qualifiers

FEATURES

1. 513
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /tissue type="brain"
 /note="Isolated from an ischemic brain"

CDS

1. 513
 /codon_start=1
 /product="bcl-x short"
 /protein_id="AAD33683.1"
 /db_xref="GI:4928688"
 /translation="MQSNRELVVDFLSVKLSQKYSWSQFSQVDEENRTEAPEETEAE
 RETPSAINGNPWSHLADSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEFLRYR
 RAPSDTSQLHITPGTAYQSFQDTFVDLYGNNAAESRKQGRFNRNFWLTGMTVAGV
 VLLGSLFSRK"

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 513;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
 |||||
 Db 78 CTGACTCCAGCTGTATCC 61

```
AF279286/c
LOCUS       AF279286               513 bp    mRNA    linear    ROD 02-JUL-2000
DEFINITION   Rattus norvegicus bcl-x short form mRNA, complete cds.
ACCESSION   AF279286
VERSION     AF279286.1  GI:8896160
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 513)
AUTHORS    Cao,G., Chen,J. and Chen,D.
TITLE      Bcl-Xs expression and its role in brain ischemia
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 513)
AUTHORS    Cao,G., Chen,J. and Chen,D.
TITLE      Direct Submission
JOURNAL    Submitted (16-JUN-2000) Neurology, University of Pittsburgh, 3500
            Terrace Street, Pittsburgh, PA 15261, USA
FEATURES    Location/Qualifiers
             1..513
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /strain="Sprague-Dawley"
                /db_xref="taxon:10116"
                /tissue_type="cerebellum"
                /dev_stage="postnatal 1 week"
             1..513
                /codon_start=1
                /product="bcl-x short form"
                /protein_id="AAF81262.1"
                /db_xref="GI:8896161"
                /translation="MSQSKRELVDVFLSKYKQKYSQFSDVENRTEAPEETEPE
                RETPSAINGNPSHLADSPAVNGATGHSSSLDAREVLPMAAVKQALRAGDEFEFLYR
                RAFSDLSLTHTPGTVYQSFEQDTFVDLYGNNTAPEKRGQERFNRLFTGWTGAVG
                VLLGSLFSRK"
ORIGIN
Query Match      100.0%; Score 18; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CDS
RESULT 9
LOCUS       S78284/c               537 bp    mRNA    linear    ROD 26-SEP-1995
DEFINITION   bcl-xshort-apoptosis inducer [rats, ovary, mRNA Partial, 537 nt].
ACCESSION   S78284
VERSION     S78284.1  GI:998483
KEYWORDS    .
SOURCE      Rattus sp.
ORGANISM    Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 537)
AUTHORS    Tilly,J.I., Tilly,K.I., Kenton,M.L. and Johnson,A.L.
TITLE      Expression of members of the bcl-2 gene family in the immature rat
            ovary: equine chorionic gonadotropin-mediated inhibition of
            granulosa cell apoptosis is associated with decreased bax and
            constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels
            Endocrinology 136 (1), 232-241 (1995)
JOURNAL    95129487
MEDLINE    7828536
PUBMED
REMARK      GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 162923] from the original journal article.
FEATURES    Location/Qualifiers
             1..537
                /organism="Rattus sp."
                /mol_type="mRNA"
                /db_xref="taxon:10118"
                /gene="bcl-xshort"
                /note="apoptosis inducer"
             2..532
                /gene="bcl-xshort"
                /note="apoptosis inducer"
                /codon_start=1
                /protein_id="AAC60702.1"
                /db_xref="GI:998484"
                /translation="PISIIKMSQSNRELVDVFLSKYKQKYSQFSDVENRTEAPE
                BETEPETPSAINGNPSHLADSPAVNGATGHSSSLDAREVLPMAAVKQALRAGDE
                FELYRRAFPSDLTSLQHLTPGTVYQSFEQDTFVDLYGNNTAPEKRGQERFNRLFTG
                MTVAGVLLGSLFSRK"
ORIGIN
Query Match      100.0%; Score 18; DB 10; Length 537;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CDS
RESULT 10
LOCUS       CQ113695               555 bp    DNA    linear    PAT 21-JAN-2004
DEFINITION   Sequence 22554 from Patent WO0157272.
ACCESSION   CQ113695
VERSION     CQ113695.1  GI:41083565
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human placenta
            Patent: WO 0157272-A 22554 09-AUG-2001;
            Aecomica, Inc. (US)
FEATURES    Location/Qualifiers
             1..555
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
                0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CDS
RESULT 11
LOCUS       CQ152574               555 bp    DNA    linear    PAT 21-JAN-2004
DEFINITION   Sequence 22596 from Patent WO0157276.
ACCESSION   CQ152574
VERSION     CQ152574.1  GI:41159924
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human bone marrow
JOURNAL      Patent: WO 0157276-A 22596 09-AUG-2001;
              Acemica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..555
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
                = 4.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTGACTCCAGCTGTATCC 18
        |||||
        487 CTGACTCCAGCTGTATCC 504

RESULT 12
LOCUS      CQ185831                      555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 17227 from Patent WO0157274.
ACCESSION  CQ185831
VERSION     CQ185831.1 GI:41180846
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human heart
JOURNAL      Patent: WO 0157274-A 17227 09-AUG-2001;
              Acemica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..555
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
                1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
                BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTGACTCCAGCTGTATCC 18
        |||||
        487 CTGACTCCAGCTGTATCC 504

RESULT 13
LOCUS      CQ235904                      555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 22743 from Patent WO0157273.
ACCESSION  CQ235904
VERSION     CQ235904.1 GI:41219182
KEYWORDS
SOURCE      Homo sapiens (human)

```

```

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
              3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
              60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
              August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
              (03.10.00)<150> US 60/236,359<151> 27 September 2000
              (27.09.00)<150> US 60/234,687<151> 21 September 2000
              (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
              Molecular Dynamics Sequence Listing Engine
JOURNAL      Patent: WO 0157273-A 22743 09-AUG-2001;
              Acemica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..555
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
                = 1.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTGACTCCAGCTGTATCC 18
        |||||
        487 CTGACTCCAGCTGTATCC 504

RESULT 14
LOCUS      CQ273477                      555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21738 from Patent WO0157277.
ACCESSION  CQ273477
VERSION     CQ273477.1 GI:41246081
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 21738 09-AUG-2001;
              Acemica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..555
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
                = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTGACTCCAGCTGTATCC 18
        |||||
        487 CTGACTCCAGCTGTATCC 504

```

RESULT 15
CQ310858
LOCUS CQ310858 555 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21963 from Patent WO0186003.
ACCESSION CQ310858
VERSION CQ310858.1 GI:41271435
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn.S.G., Hanzel.D.K., Chen.W. and Rank.D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human lung
JOURNAL Patent: WO 0186003-A 21963 15-NOV-2001;
Neomica, Inc. (US)
FEATURES
source
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACTCCAGCTGTATCC 18
|||||
Db 487 CTGACTCCAGCTGTATCC 504
Search completed: February 4, 2005, 23:30:41
Job time : 432.664 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169A-8
Perfect score: 18
Sequence: 1 ctgactccagctgtatcc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AAZ46978	Bcl-XL mr
2	18	100.0	65	ABN55935	Mouse spl
3	18	100.0	555	ABA73433	Human foe
4	18	100.0	555	Aai53868	Probe #22
5	18	100.0	555	ABA38761	Probe #17
6	18	100.0	555	AAK48039	Human bon
7	18	100.0	555	AAK21876	Human bra
8	18	100.0	555	ABS47753	Human liv
9	18	100.0	555	ABS21972	Human gen
10	18	100.0	559	ACH73889	Human gen
11	18	100.0	564	ACH87595	Human gen
12	18	100.0	600	ABA60917	Human foe
13	18	100.0	600	AAI40812	Probe #94
14	18	100.0	600	ABA28894	Probe #73
15	18	100.0	600	AAK35096	Human bon
16	18	100.0	600	AAK09207	Human bra
17	18	100.0	600	ABA34848	Human liv
18	18	100.0	600	ABS09558	Human gen
c 19	18	100.0	600	ADH52636	Chinese h
c 20	18	100.0	660	ADH52638	Chinese h
c 21	18	100.0	660	ADH52640	Chinese h

ALIGNMENTS

RESULT 1
AAZ46978
ID AAZ46978 standard; DNA; 18 BP.
XX AC AAZ46978;
XX AC

DT 14-APR-2000 (first entry)

DE Bcl-XL mRNA specific antisense oligo H.

KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;
lung; bladder; bcl-2; vascular lesion; antisense; ss.

XX Homo sapiens.

OS WO200001393-A2.

XX 13-JAN-2000.

XX 02-JUL-1999; 99WO-US015250.

XX 02-JUL-1998; 98US-00109614.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Stein CA;

XX WPI; 2000-137140/12.

PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

XX Claim 1; Fig 1; 69pp; English.

XX The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

Abt09346 Phase-1 R
Aah43464 cDNA cion
Adm45994 Human apo
Aaq81699 Human thy
Abz83507 Toxicolog
Adi32132 Human CDN
Adg5218 Human Bcl
Adf30926 Human Bcl
Adg5209 Human Bcl
Adh52632 Chinese h
Aaq81698 Human thy
Aat40079 Bcl-XL ge
Aaz93614 Bcl-x gen
Aas15189 Human bcl
Aac90810 Human Bcl
Abk84766 Human CDN
Abt16641 Human bcl
Add56779 Human bcl
Aad64187 Human bcl
Adi32104 Human CDN
Adh52630 Human ant
Ado19990 Human PRO
Adp13351 Renal cel
Aas00247 Bcl-XL-DT

CC lesions. They can also be included with a carrier (and optionally tetra
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
 CC pharmaceutical compositions, useful as above. Sequences AA246971-983
 CC represent antisense oligos specific for the bcl-X1 mRNA

XX SQ Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18
 |||||
 Db 1 CTGACTCCAGCTGTATCC 18

RESULT 2
 ABN55935/c
 ID ABN55935 standard; DNA; 65 BP.
 XX AC ABN55935;
 XX DT 15-JUL-2002 (first entry)
 XX DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:28683.
 XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 XX KW splice variant; transcriptome; oligonucleotide library; ss.
 XX OS Mus musculus.
 XX PN WO200210449-A2.
 XX PD 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB001903.
 XX 28-JUL-2000; 2000US-0221607P.
 XX 02-MAY-2001; 2001US-0287724P.
 XX (COMP-) COMPUGEN INC.
 XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX WPI; 2002-257383/30.
 XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.

XX Example 1; SEQ ID NO 28683; 47pp; English.
 XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridizing selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the

CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 65 BP; 19 A; 12 C; 20 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 65;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGACTCCAGCTGTATCC 18
 |||||
 Db 31 CTGACTCCAGCTGTATCC 14

RESULT 3
 ABA73433
 ID ABA73433 standard; DNA; 555 BP.
 XX AC ABA73433;
 XX DT 01-FEB-2002 (first entry)
 XX DE Human foetal liver single exon nucleic acid probe #21738.
 XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX OS Homo sapiens.
 XX PN WO200157277-A2.
 XX PD 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000669.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human foetal liver.
 XX Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.
 XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human foetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGACTCCAGCTGTATCC 18
 |||||
 Db 487 CTGACTCCAGCTGTATCC 504


```

RESULT 4
AAI53868
ID AAI53868 standard; DNA; 555 BP.
XX AC AAI53868;
XX DT 17-OCT-2001 (first entry)
XX DE Probe #22554 used to measure gene expression in human placenta sample.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX PS Claim 25; SEQ ID NO 22554; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP).
XX CC The present sequence is one such probe. The probes are useful for
XX CC producing a microarray for predicting, measuring and displaying gene
XX CC expression in samples derived from human placenta. The probes are useful
XX CC for antenatal diagnosis of human genetic disorders
XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
Db 487 CTGACTCCAGCTGTATCC 504

RESULT 5
ABA38761
ID ABA38761 standard; DNA; 555 BP.
XX AC ABA38761;
XX DT 23-JAN-2002 (first entry)
XX DE Probe #17227 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.
XX OS Homo sapiens.

```

```

XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX PS Claim 4; SEQ ID NO 17227; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease. Note: The sequence data for this patent did not
XX CC form part of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
Db 487 CTGACTCCAGCTGTATCC 504

RESULT 6
AAK48039
ID AAK48039 standard; DNA; 555 BP.
XX AC AAK48039;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 22596.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.

```


CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACTCCAGCTGTATCC 18
Db 487 CTGACTCCAGCTGTATCC 504
RESULT 9
ABS21972
ID ABS21972 standard; DNA; 555 BP.
XX
AC ABS21972;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 21963.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-0060840B.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 4; SEQ ID NO 21963; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridize at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe open reading frame of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACTCCAGCTGTATCC 18
Db 487 CTGACTCCAGCTGTATCC 504
RESULT 10
ACH73889
ID ACH73889 standard; DNA; 559 BP.
XX
AC ACH73889;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon probe #7084.
XX
KW Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for

```

PT surveying tissues.
XX
XX
XX Claim 15; SEQ ID NO 7084; 80pp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX SQ Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 18; DB 12; Length 559;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 CTGACTCCAGCTGTATCC 18
| | | | | | | | | | | | | | | |
Db 82 CTGACTCCAGCTGTATCC 99
| | | | | | | | | | | | | | | |
RESULT 11
ID ACH87595 standard; DNA; 564 BP.
XX
XX ACH87595;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon probe #20790.
XX
XX Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
XX
XX US2003194704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX

```

```

XX
XX
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX
XX Claim 1; SEQ ID NO 20790; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterising
XX alternative splicing events, in detecting and characterising gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids,
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX SQ Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 18; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 CTGACTCCAGCTGTATCC 18
| | | | | | | | | | | | | | | |
Db 487 CTGACTCCAGCTGTATCC 504
| | | | | | | | | | | | | | | |
RESULT 12
ID ABA60917 standard; DNA; 600 BP.
XX
XX ABA60917;
XX
XX 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #9222.
XX

```

KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX Homo sapiens.
 OS WO200157277-A2.
 PN 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000669.
 PF 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.
 PS The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 600;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CTGACTCCAGCTGTATCC 18
 Db 506 CTGACTCCAGCTGTATCC 523
 RESULT 13
 AAI40812
 ID AAI40812 standard; DNA; 600 BP.
 XX
 AC AAI40812;
 XX 17-OCT-2001 (first entry)
 DT Probe #9498 used to measure gene expression in human placenta sample.
 DE Probe; microarray; human; placenta; antenatal diagnosis;
 XX genetic disorder; ss.
 KW Homo sapiens.
 OS WO200157272-A2.
 PN 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000663.
 PF 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX Claim 25; SEQ ID NO 9498; 654pp; English.
 PS The present invention relates to single exon nucleic acid probes (SENPs).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders
 XX
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 600;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CTGACTCCAGCTGTATCC 18
 Db 506 CTGACTCCAGCTGTATCC 523
 RESULT 14
 ABA28894
 ID ABA28894 standard; DNA; 600 BP.
 XX
 AC ABA28894;
 XX 23-JAN-2002 (first entry)
 DT Probe #7360 for gene expression analysis in human heart cell sample.
 DE Human; gene expression; heart; microarray; vascular system; probe;
 XX cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 OS Homo sapiens.
 XX WO200157274-A2.
 PN 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000666.
 PF 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX Claim 1; SEQ ID NO 7360; 530pp; English.
 PS

XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
Db 506 CTGACTCCAGCTGTATCC 523

RESULT 15

AAK35096
ID AAK35096 standard; DNA; 600 BP.

XX AC AAK35096;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 9653.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention

XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
Db 506 CTGACTCCAGCTGTATCC 523

Search completed: February 4, 2005, 21:52:43
Job time : 233.23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-8
Perfect score: 18
Sequence: 1 ctgactccagctgtatcc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gsl1: *
9: gb_gsl2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	279	2	AW247015
C 2	18	100.0	287	5	BY236510
C 3	18	100.0	313	6	CF171262
C 4	18	100.0	320	5	BY220922
C 5	18	100.0	322	2	AW125200
C 6	18	100.0	325	5	BY191347
C 7	18	100.0	327	5	BY209882
C 8	18	100.0	336	5	BY219527
C 9	18	100.0	339	1	AA232598
C 10	18	100.0	341	5	BY176914
C 11	18	100.0	344	2	BB869154
C 12	18	100.0	348	5	BY010071
C 13	18	100.0	350	5	BY058101
C 14	18	100.0	353	5	BY016163
C 15	18	100.0	355	5	BY180189
C 16	18	100.0	355	5	BY212491
C 17	18	100.0	356	5	BY180646
C 18	18	100.0	357	2	BB870590
C 19	18	100.0	358	5	BY203613
C 20	18	100.0	361	5	BY176753
C 21	18	100.0	363	5	BY221240
C 22	18	100.0	363	5	BY293078
C 23	18	100.0	367	2	BB843018
C 24	18	100.0	368	5	BY178528

C 25	18	100.0	369	5	BY174511
C 26	18	100.0	374	2	BB844512
C 27	18	100.0	374	5	BY055234
C 28	18	100.0	378	2	BB871778
C 29	18	100.0	382	2	BB842471
C 30	18	100.0	382	4	BM855440
C 31	18	100.0	391	2	BE253353
C 32	18	100.0	391	5	BY096186
C 33	18	100.0	391	6	CB775315
C 34	18	100.0	394	6	CD540521
C 35	18	100.0	395	4	BI030877
C 36	18	100.0	402	6	CB769704
C 37	18	100.0	407	7	CN422267
C 38	18	100.0	408	5	BY298104
C 39	18	100.0	408	6	CA558426
C 40	18	100.0	414	2	BF523847
C 41	18	100.0	421	4	BM844286
C 42	18	100.0	421	6	CF145335
C 43	18	100.0	422	5	BY281787
C 44	18	100.0	425	5	BY287181
C 45	18	100.0	431	6	CA896103

ALIGNMENTS

RESULT 1
AW247015/c
LOCUS 2822471.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822471 5',
DEFINITION mRNA sequence.
ACCESSION AW247015
VERSION AW247015.1 GI:6590008
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 279)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2822471.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project. Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu
Plate: LLCM9 row: H column: 24
High quality sequence stop: 199.
Location/Qualifiers
1. 279
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822471"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18
|||||
Db 134 CTGACTCCAGCTGTATCC 117

RESULT 2

BY236510/c
LOCUS BY236510 RIKEN full-length enriched, adult inner ear Mus musculus
DEFINITION cDNA clone F930048G15 5', mRNA sequence.

ACCESSION BY236510
VERSION BY236510.1 GI:26417686
KEYWORDS EST.

SOURCE

Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 287)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schoenbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gliss, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Santelina, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L. G., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

TITLE

Of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Azawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN,
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National
Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose
assistance we gratefully acknowledge. Please visit our web site
(<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

1. .287
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F930048G15"
/tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACTCCAGCTGTATCC 18
|||||
Db 138 CTGACTCCAGCTGTATCC 121

RESULT 3

LOCUS

CF171262/c
CF171262 313 bp mRNA linear EST 25-JUL-2003
B0840B09-5 NIA Mouse Newborn Kidney cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0840B09 IMAGE:30471284 5', mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

Piao, Y., Ko, N. T., Lim, M. K. and Ko, M. S. H.
Subtraction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method

JOURNAL

MEDLINE

PUBMED

COMMENT

Genome Res. 11 (9), 1553-1558 (2001)
21429098
11544199
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0840 row: B column: 09
Seq primer: M3 Reverse
High quality sequence stop: 313
POLYA=NO.

FEATURES

source

Location/Qualifiers
1. .313
/organism="Mus musculus"


```

/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="NIA:B0840B09 IMAGE:30471284"
/dev_stage="Newborn Kidney"
/lab_host="DH10B"
/clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long
1)"
/Note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
In brief, double-stranded cDNAs were synthesized with an
Oligo(dT) primer (Invitrogen):
5'-pGACTAGTTCAGTCGAGCGGCCGCTTTT-3' from
26 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Loner-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 3.0 kb. The library was
constructed by Yulan Piao."

```

ORIGIN

```

Query Match 100.0%; Score 18; DB 6; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CTGACTCCAGCTGTATCC 18

```

```

Db 45 CTGACTCCAGCTGTATCC 28

```

RESULT 4

```

BY220922/c

```

DEFINITION

```

BY220922 RIKEN full-length enriched, activated spleen Mus musculus
cDNA clone F830217H02 5', mRNA sequence.

```

ACCESSION

```

BY220922

```

VERSION

```

BY220922.1 GI:26402025

```

KEYWORDS

```

EST.

```

SOURCE

```

Mus musculus (house mouse)

```

ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE

```

1 (bases 1 to 320)

```

AUTHORS

```

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konegaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

```

```

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Shisikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
PUBMED
12466851

```

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

```

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

```

```

Email: genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Wataniki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

```

```

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

```

FEATURES

source

```

1..320

```

```

/organism="Mus musculus"

```

```

/mol_type="mRNA"

```

```

/strain="NOD"

```

```

/db_xref="taxon:10090"

```

```

/clone="F830217H02"

```

```

/tissue_type="activated spleen"

```

```

/clone_lib="RIKEN full-length enriched, activated spleen"

```

ORIGIN

```

Query Match 100.0%; Score 18; DB 5; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CTGACTCCAGCTGTATCC 18

```

```

Db 276 CTGACTCCAGCTGTATCC 259

```

RESULT 5

```

AW125200/c

```

LOCUS

```

AW125200

```

DEFINITION

```

UI-M-BH2.1-aps-a-07-0-UI.s1 NIH BMAP M.S3.1 Mus musculus cDNA clone

```

```

UI-M-BH2.1-aps-a-07-0-UI 3', mRNA sequence.

```

```

322 bp mRNA linear EST 22-OCT-1999

```

ACCESSION AW125200
 VERSION AW125200.1 GI:6100730
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE 1 (bases 1 to 322)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 889548
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mst@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone Distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
 Seq primer: M13 Forward
 POLYA=yes.

Location/Qualifiers
 1..322
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UI-M-BH2.1-aps-a-07-0-UI"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH BMAP M S3.1"
 /note="Vector: p7735-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP M S3.1 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH BMAP M S3.1, NIH BMAP M S2, NIH BMAP M S1. The subtracted library (NIH BMAP M S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH BMAP M S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH BMAP M S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH BMAP M S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_TISSUE=brain-stems
 TAG_LIB=NIH BMAP_M_S3.1
 TAG_SEQ=TCGA"

FEATURES
 source

Query Match 100.0%; Score 18; DB 2; Length 322;

ORIGIN

Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18
 Db 310 CTGACTCCAGCTGTATCC 293
 ||||||||||||||||
 ||||||||||||||||

RESULT 6
 BY191347/c
 LOCUS
 DEFINITION
 BY191347 RIKEN full-length enriched, MOD-derived cDNA clone F630320F03 5', mRNA
 dendritic cells Mus musculus cDNA clone F630320F03 5', mRNA
 sequences.
 BY191347
 BY191347.1 GI:26366310
 EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE Eukaryota; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 325)
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batailov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Saitanin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 12466851
 22354683
 12466851
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Tsurumi-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

```

1. 325
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630320F03"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"

```

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18

Db 263 CTGACTCCAGCTGTATCC 246

RESULT 7

LOCUS

BY209882/c 327 bp mRNA linear EST 10-DEC-2002
 BY209882 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
 cells Mus musculus cDNA clone F730312F08 5', mRNA sequence.

ACCESSION

VERSION BY209882.1 GI:26390370

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 327)

REFERENCE

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
 Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gariboldi, M., Glessi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
 Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Nunata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
 Petrovsky, N., Pilla, R., Pontius, J. U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J. C., Reid, J., Ring, B. Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yangisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hata, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source

```

1. 327
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F730312F08"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, B6-derived CD11
+ve dendritic cells"

```

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18

Db 288 CTGACTCCAGCTGTATCC 271

RESULT 8

LOCUS

BY219527/c 336 bp mRNA linear EST 10-DEC-2002
 BY219527 RIKEN full-length enriched, activated spleen Mus musculus
 cDNA clone F830115M14 5', mRNA sequence.

ACCESSION

BY219527

VERSION BY219527.1 GI:26400547
 EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 336)
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaado, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Gojibori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Ciothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Glissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Negashima, T., Numata, K., Okido, T., Favan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Varardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, B.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)
 MEDLINE 22354683
 PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Akakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

FEATURES
 Source
 Location/Qualifiers
 1..336
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="M0D"
 /db_xref="taxon:10090"
 /clone="F830115M14"
 /tissue_type="activated spleen"
 /clone_lib="RIKEN full-length enriched, activated spleen"

ORIGIN
 Query Match 100.0%; Score 18; DB 5; Length 336;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CTGACTCCAGCTGTATCC 18
 |||||
 278 CTGACTCCAGCTGTATCC 261

RESULT 9
 AA232598/c
 LOCUS
 DEFINITION zr28c08.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens
 CDNA clone IMAGE:664718 5', similar to TR:G998484 G998484
 BCL-XSHTO=APOPTOSIS INDUCER ; mRNA sequence.
 AA232598
 VERSION AA232598.1 GI:1855453
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 339)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J., Trevas, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 8889549
 97044478
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 175.
 Location/Qualifiers
 1..339
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:5426748"
 /db_xref="taxon:9606"
 /clone="IMAGE:664718"
 /tissue_type="neuroepithelial cells"
 /dev_stage="Ntera-2 neuroepithelial cells"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene NT2 neuronal precursor 937230"
 /note="Organ: brain; Vector: pBluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Uninduced, exponentially growing neuroepithelial cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGGAG
3' -3' adaptor sequence: 5' CTCAGTGTGTGTGTGTGTGTGT 3'

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18

Db 300 CTGACTCCAGCTGTATCC 283

RESULT 10

BY176914/c
LOCUS
DEFINITION BY176914 RIKEN full-length enriched, NOD-derived CD11c +ve
dendritic cells Mus musculus cDNA clone F630021E08 5', mRNA
sequence.

ACCESSION

VERSION BY176914.1 GI:26313560

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Okazaki, Y., Furuno, M., Saito, R., Suzuki, H., Yamanaka, I.,
Nikaido, I., Osato, N., Saito, R., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Kiyosawa, H., Yagi, K., Kato, M., Saito, R., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bratt, D., Brusci, V.,
Choithia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,
Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Vezardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yangisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL

MEDLINE

PUBMED

COMMENT

Nature 420, 563-573 (2002)
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC Building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES

source

Location/Qualifiers
1..341
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630021E08"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 341;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18

Db 294 CTGACTCCAGCTGTATCC 277

RESULT 11

BB869154/c

LOCUS

DEFINITION BB869154 RIKEN full-length enriched, pooled tissues, intestinal
mucosa, etc. Mus musculus cDNA clone G630011A21 5', mRNA sequence.

ACCESSION BB869154.1 GI:17115364

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 344)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R.,

Okazaki, Y., Okido, T., Saito, K., Sakai, C., Sakai, K., Sakazume, N.,

Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
2001)

Unpublished (2001)

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

<p>Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsic.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuura, S., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.</p>	<p>REFERENCE AUTHORS</p>	<p>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 348) Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Ootani, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustigich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Negashima, T., Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)</p>	<p>TITLE</p>	<p>JOURNAL</p>	<p>MEDLINE</p>	<p>PUBMED</p>	<p>COMMENT</p>	<p>CONTACT: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsic.riken.jp, URL: http://genome.gsc.riken.jp/ Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for further details. Location/Qualifiers 1. .348 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="G730016N07" /tissue_type="lung"</p>	<p>FEATURES source</p>	<p>Query Match 100.0%; Score 18; DB 2; Length 344; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>Qy 1 CTGACTCCAGCTGTATCC 18 Db 219 CTGACTCCAGCTGTATCC 202</p>	<p>RESULT 12 BY010071/c LOCUS DEFINITION BY010071 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus musculus CDNA clone G730016N07 5', mRNA sequence. ACCESSION BY010071.1 GI:26070320 VERSION BY010071.1 KEYWORDS Mus musculus (house mouse) SOURCE Mus musculus ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p>
---	-------------------------------	---	--------------	----------------	----------------	---------------	----------------	---	-----------------------------	---	---	---

```

/cell_line="RCB-0558 LLC"
/clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
cDNA"

ORIGIN
Query Match      100.0%; Score 18; DB 5; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGACTCCAGCTGTATCC 18
    |||||
Db 288 CTGACTCCAGCTGTATCC 271

RESULT 13
BY058101/c
LOCUS
DEFINITION
  BY058101 RIKEN full-length enriched, TIB-55 BB88 Mus musculus cDNA
  clone 1730095E04 5', mRNA sequence.

ACCESSION
  BY058101
VERSION
  BY058101.1 GI:26163549
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 350)
  Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
  Okazaki, Y., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
  Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
  Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
  Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
  Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
  Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
  Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
  Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
  Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
  Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
  Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
  Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
  Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
  Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
  Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
  Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
  Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
  Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
  Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
  Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
  Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
  Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
  Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
  Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
  Rogers, J., Birney, E. and Hayashizaki, Y.
  Analysis of the mouse transcriptome based on functional annotation
  of 60,770 full-length cDNAs
  Nature 420, 563-573 (2002)
  22354683
  12466851
  Contact: Yoshihide Hayashizaki
  Laboratory for Genome Exploration Research Group, RIKEN Genomic
  Sciences Center (GSC), Yokohama Institute
  The Institute of Physiological and Chemical Research (RIKEN)
  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
  Tel: 81-45-503-9222
  Fax: 81-45-503-9216
  Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
  Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
  Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
  Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
  Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
  Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
  Hayashizaki, Y. Direct Submission

```

```

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
  source
  Location/Qualifiers
    1..350
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="BALB/c"
      /db_xref="taxon:10090"
      /cnames="I730095E04"
      /cell_line="TIB-55 BB88"
      /clone_lib="RIKEN full-length enriched, TIB-55 BB88"
ORIGIN
Query Match      100.0%; Score 18; DB 5; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGACTCCAGCTGTATCC 18
    |||||
Db 280 CTGACTCCAGCTGTATCC 263

RESULT 14
BY016163/c
LOCUS
DEFINITION
  BY016163 RIKEN full-length enriched, mammary gland RCB-0526
  Jyg-MC(A) cDNA Mus musculus cDNA clone G830015P06 5', mRNA
  sequence.
ACCESSION
  BY016163
VERSION
  BY016163.1 GI:26076412
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 353)
  Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
  Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
  Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
  Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
  Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
  Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
  Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
  Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
  Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
  Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
  Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
  Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
  Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
  Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
  Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
  Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
  Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
  Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
  Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
  Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
  Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
  Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
  Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
  Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
  Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
  Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
  Rogers, J., Birney, E. and Hayashizaki, Y.
  Analysis of the mouse transcriptome based on functional annotation
  of 60,770 full-length cDNAs
  Nature 420, 563-573 (2002)
  22354683
  12466851
  Contact: Yoshihide Hayashizaki
  Laboratory for Genome Exploration Research Group, RIKEN Genomic
  Sciences Center (GSC), Yokohama Institute
  The Institute of Physiological and Chemical Research (RIKEN)
  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
  Tel: 81-45-503-9222
  Fax: 81-45-503-9216
  Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
  Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
  Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
  Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
  Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
  Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
  Hayashizaki, Y. Direct Submission

```


Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Comment: Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

1..353

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="G830015P06"

/tissue_type="mammary gland"

/cell_line="RCB-0526 Jyg-MC(A)"

/clone_lib="RIKEN full-length enriched, mammary gland RCB-0526 Jyg-MC(A) cDNA"

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18

|||||

Db 296 CTGACTCCAGCTGTATCC 279

RESULT 15

BY180189/c

LOCUS

DEFINITION

BY180189 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630038P12 5', mRNA sequence.

ACCESSION

BY180189

VERSION

BY180189.1 GI:26316835

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 353)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaïdo, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrester, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Comment: Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.


```
FEATURES
source
Location/Qualifiers
1. .355
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630038P12"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"

ORIGIN
Query Match 100.0%; Score 18; DB 5; Length 355;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18
|||
Db 263 CTGACTCCAGCTGTATCC 246

Search completed: February 5, 2005, 08:11:48
Job time : 2149.2 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-9
Perfect score: 18
Sequence: 1 ggtctccatctccgattc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ats.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235157
2	18	100.0	18	6	BD235175
3	18	100.0	18	6	BD235176
4	18	100.0	512	6	CQ727769 Sequence
5	18	100.0	555	6	CQ113695
6	18	100.0	555	6	CQ152574
7	18	100.0	555	6	CQ185831
8	18	100.0	555	6	CQ235904
9	18	100.0	555	6	CQ273477
10	18	100.0	555	6	CQ310858
11	18	100.0	555	6	CQ347773
12	18	100.0	600	6	CQ100639
13	18	100.0	600	6	CQ139631
14	18	100.0	600	6	CQ175964
15	18	100.0	600	6	CQ222999
16	18	100.0	600	6	CQ260961
17	18	100.0	600	6	CQ298444
18	18	100.0	600	6	CQ335104
19	18	100.0	636	6	BD097037

c 20	18	100.0	702	6	BD084108
c 21	18	100.0	702	6	BD102202
c 22	18	100.0	702	9	BT007208
c 23	18	100.0	702	12	BT008248
c 24	18	100.0	723	9	HSU72398
c 25	18	100.0	737	6	AR054022
c 26	18	100.0	737	6	AR172595
c 27	18	100.0	737	6	IS2012
c 28	18	100.0	737	6	AR371662
c 29	18	100.0	737	6	AR380913
c 30	18	100.0	737	9	HSBCLXS
c 31	18	100.0	747	6	AX127722
c 32	18	100.0	926	6	AR054021
c 33	18	100.0	926	6	AR118504
c 34	18	100.0	926	6	AR124952
c 35	18	100.0	926	6	AR144311
c 36	18	100.0	926	6	AR172594
c 37	18	100.0	926	6	BD243042
c 38	18	100.0	926	6	CQ765842
c 39	18	100.0	926	6	E58777
c 40	18	100.0	926	6	IS2011
c 41	18	100.0	926	6	AR380885
c 42	18	100.0	926	6	AX839772
c 43	18	100.0	926	6	AX925686
c 44	18	100.0	926	9	HSBCLXL
c 45	18	100.0	1236	6	AX085490

ALIGNMENTS

RESULT 1
BD235157
LOCUS BD235157 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION BD235157
VERSION BD235157.1 GI:33044927
KEYWORDS JP 2002519048-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Stein,C.A.
TITLE Oligonucleotide inhibitors of bcl-xL
JOURNAL Patent: JP 2002519048-A 9 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT OS Artificial Sequence
PN JP 2002519048-A/9
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN
PC
C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence',
Location/Qualifiers
1..18
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

FEATURES

source

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GGTCTCCATCTCCGATTC 18
|||||

```

Db      1  GGTCTCCATCTCCGATTC 18

RESULT 2
BD235175
LOCUS      18 bp      DNA
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235175
VERSION     BD235175.1 GI:33044945
KEYWORDS   JP 2002519048-A/27.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Stein, C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 27 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/27
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC
           C12N15/09,A61K9/127,A61K31/711,A61K31/712,A61K31/7125, PC
           A61K47/42,
           PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
           CC ANTISENSE OLIGONUCLEOTIDE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           FH Key Location/Qualifiers
           FT misc_binding (1)..(4)
           FT misc_binding (5)..(7)
           FT misc_binding (9)..(10)
           FT misc_binding (11)..(12)
           FT misc_binding (15)..(18)
           FT modified_base (3)..(3)
           FT modified_base (4)..(4)
           FT modified_base (6)..(7)
           FT modified_base (5)..(5)
           FT modified_base (9)..(9)
           FT modified_base (10)..(10)
           FT modified_base (11)..(11)
           FT modified_base (12)..(13)
           FT modified_base (16)..(17).
FEATURES
  source
    1..18
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
ORIGIN
  Query Match 100.0%; Score 18; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 59;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTCTCCATCTCCGATTC 18
        |||||
DB      1  GGTCTCCATCTCCGATTC 18

RESULT 4
CQ272769/c
LOCUS      512 bp      DNA
DEFINITION Sequence 13703 from Patent WO02068579.
ACCESSION  CQ272769
VERSION     CQ272769.1 GI:42294740
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1
AUTHORS    Venter C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE      Kits, such as nucleic acid arrays, comprising a majority of
           humanexons or transcripts, for detecting expression and other uses
           thereof
JOURNAL    Patent: WO 02068579-A 13703 06-SEP-2002;
           PE Corporation (NY) (US)
FEATURES
  Location/Qualifiers
    1..18
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
ORIGIN
  Query Match 100.0%; Score 18; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 59;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTCTCCATCTCCGATTC 18
        |||||
DB      1  GGTCTCCATCTCCGATTC 18

```

```

source
1. 512
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 512;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
    |||||
Db 275 GGTCTCCATCTCCGATTC 258

RESULT 5
CQ113695
LOCUS      CQ113695          555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 22554 from Patent WO0157272.
ACCESSION  CQ113695
VERSION     CQ113695.1 GI:41083565
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
JOURNAL    Patent: WO 0157272-A 22554 09-AUG-2001;
Aecomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
    |||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 6
CQ152574
LOCUS      CQ152574          555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 22596 from Patent WO0157276.
ACCESSION  CQ152574
VERSION     CQ152574.1 GI:41159924
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL    Patent: WO 0157276-A 22596 09-AUG-2001;
Aecomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
    |||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 7
CQ185831
LOCUS      CQ185831          555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 17227 from Patent WO0157274.
ACCESSION  CQ185831
VERSION     CQ185831.1 GI:41180846
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
JOURNAL    Patent: WO 0157274-A 17227 09-AUG-2001;
Aecomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
    |||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 8
CQ235904
LOCUS      CQ235904          555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 22743 from Patent WO0157273.
ACCESSION  CQ235904
VERSION     CQ235904.1 GI:41219182
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE      HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000

```

(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 22743 09-AUG-2001;
Aeomica, Inc. (US)

FEATURES
source
Location/Qualifiers
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
= 1.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18
|||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 9
LOCUS CQ273477 555 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21738 from Patent WO0157277.
ACCESSION CQ273477
VERSION CQ273477.1 GI:41246081
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human fetal liver
JOURNAL Patent: WO 0157277-A 21738 09-AUG-2001;
Aeomica, Inc. (US)

FEATURES
source
Location/Qualifiers
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
= 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18
|||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 10
LOCUS CQ310858 555 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21963 from Patent WO0186003.
ACCESSION CQ310858
VERSION CQ310858.1 GI:41271435
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human lung
Patent: WO 0186003-A 21963 15-NOV-2001;
Aeomica, Inc. (US)

FEATURES
source
Location/Qualifiers
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18
|||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 11
LOCUS CQ347773 555 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21867 from Patent WO0157275.
ACCESSION CQ347773
VERSION CQ347773.1 GI:41296844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 21867 09-AUG-2001;
Aeomica, Inc. (US)

FEATURES
source
Location/Qualifiers
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18
|||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 12
LOCUS CQ100639 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 9498 from Patent WO0157272.
ACCESSION CQ100639
VERSION CQ100639.1 GI:41069665
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 9498 09-AUG-2001;
Aecomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL = 0.99"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCATCTCCGATTC 18
|||||
Db 443 GGCTCCATCTCCGATTC 460

RESULT 13
LOCUS CQ139631 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 9653 from Patent WO0157276.
ACCESSION CQ139631
VERSION CQ139631.1 GI:41097003
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 9653 09-AUG-2001;
Aecomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL = 4.7"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCATCTCCGATTC 18
|||||
Db 443 GGCTCCATCTCCGATTC 460

RESULT 14
LOCUS CQ175964 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 7360 from Patent WO0157274.
ACCESSION CQ175964
VERSION CQ175964.1 GI:41170703
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for

analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 7360 09-AUG-2001;
Aecomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCATCTCCGATTC 18
|||||
Db 443 GGCTCCATCTCCGATTC 460

RESULT 15
LOCUS CQ222999 600 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 9838 from Patent WO0157273.
ACCESSION CQ222999
VERSION CQ222999.1 GI:41205280
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000 (03.10.00)<150> US 60/236,359<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine
JOURNAL Patent: WO 0157273-A 9838 09-AUG-2001;
Aecomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL = 1.7"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCATCTCCGATTC 18
|||||
Db 443 GGCTCCATCTCCGATTC 460

Search completed: February 4, 2005, 23:30:41
Job time : 432.664 secs

ORIGINAL LEFT BLANK

SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	18	100.0	18	3	AAZ46979	Aaz46979 Bcl-X1 mR
2	18	100.0	555	4	ABA73433	Aba73433 Human foe
3	18	100.0	555	4	RAI53868	Rai53868 Probe #22
4	18	100.0	555	4	AAK38761	Aak38761 Probe #17
5	18	100.0	555	4	AAK48039	Aak48039 Human bon
6	18	100.0	555	4	AAK21876	Aak21876 Human bra
7	18	100.0	555	4	ABS47753	Abs47753 Human liv
8	18	100.0	555	6	ABS21972	Abs21972 Human gen
9	18	100.0	559	12	ACH73889	Ach73889 Human gen
10	18	100.0	564	12	ACH87595	Ach87595 Human gen
11	18	100.0	600	4	ABA60917	Aba60917 Human foe
12	18	100.0	600	4	AAI40812	Aai40812 Probe #94
13	18	100.0	600	4	ABA28894	Aba28894 Probe #73
14	18	100.0	600	4	AAK35096	Aak35096 Human bon
15	18	100.0	600	4	AAK09207	Aak09207 Human bra
16	18	100.0	600	4	ABS34848	Abs34848 Human liv
17	18	100.0	600	6	ABS09558	Abs09558 Human gen
18	18	100.0	636	4	AHA45169	Aha45169 Mutant bc
19	18	100.0	702	5	AAH43464	Aah43464 cDNA clon
20	18	100.0	702	12	ADM45994	Adm45994 Human apo
21	18	100.0	737	2	AAQ81699	Aaq81699 Human thy

ALIGNMENTS

RESULT 1

AAZ46979

ID AAZ46979 standard; DNA; 18 BP.

XX

AC
AAZ46979;

XX
DT 14-SEP-2000 (F:VGT CNT-WT)

DT 14-APR-2000 (first entry)
XX

DE Bcl-1-X1 mRNA specific antisense

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2

Anti-apoptotic protein; bcl-xL

KW lung; bladder; bcl-2; vascular

3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527

OS Homo sapiens.

XX
PN
W0200001393-32

FN
XX
W0200001393-AZ.

PD 13-JAN-2000.

XX
CT

PF 02-JUL-1999; 99WO-US015250.

XX
XX

PR 02-JUL-1998; 98US-00109614.

XX
DA
/ITVCO) INTY. COI TMBT A NEW VOPZ

PA (UYCS) UNIV COLUMBIA NEW YORK
XX

XX PI Stein CA:

[illegible]

DR WPI; 2000-137140/12.

XX

PT New antisense oligonucleotides

PT xL, useful for reducing bcl-xL

PT. or in vascular cells to promote

XX
ps
Claim 1: Fig 1: 60nm. English

FS
XX
СТАМ 1; FIG 1; 69PP; ENGLISH.

CC The invention provides antisense

which reduce or eliminate expression of the invasion proteins and

CC xL. The oligonucleotides can be

bcl-xL production to treat can

prostate, lung or bladder cancer.

CC bases with a C-5 propynyl pyrrolidine

33 such treatment The oligonucleotide family

cells to reduce bcl-xL production
such treatment: the oligonucleo-

)
)
)
)
)
4
2

)
)
4
)
2

)
)
3
3
0
4

)
)
)

0
4
4
0
)

)
)
)

CC lesions. They can also be included with a carrier (and optionally tetra
CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
CC represent antisense oligos specific for the bcl-X1 mRNA

XX
SQ Sequence 18 BP; 2 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18
|||||
Db 1 GGTCCTCATCTCCGATTC 18

RESULT 2
ABA73433
ID ABA73433 standard; DNA; 555 BP.

XX
AC ABA73433;

DT 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #21738.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human foetal liver.

XX Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human foetal liver. The

XX present sequence is a single exon nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences

RESULT 3
AAI53868
ID AAI53868 standard; DNA; 555 BP.
XX
AC AAI53868;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #22554 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 25; SEQ ID NO 22554; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).

XX The present sequence is one such probe. The probes are useful for

XX producing a microarray for predicting, measuring and displaying gene

XX expression in samples derived from human placenta. The probes are useful

XX for antenatal diagnosis of human genetic disorders

XX Query Match 100.0%; Score 18; DB 4; Length 555;

XX Best Local Similarity 100.0%; Pred. No. 39;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18

Db 424 GGTCCTCATCTCCGATTC 441

RESULT 4

ABA38761

ID ABA38761 standard; DNA; 555 BP.

XX
AC ABA38761;

XX
DT 23-JAN-2002 (first entry)

XX Probe #17227 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease; ss.

Single exon nucleic acid probes for analyzing gene expression in human brains.

```
XX Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
PS
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTCCATCTCCGATTC 18
DB 424 GGCTCCATCTCCGATTC 441
RESULT 7
ABS47753
ID ABS47753 standard; DNA; 555 BP.
XX
AC ABS47753;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID NO 22743.
XX
KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-48898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 4; SEQ ID NO 22743; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (i) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
```

```
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTCCATCTCCGATTC 18
DB 424 GGCTCCATCTCCGATTC 441
RESULT 8
ABS21972
ID ABS21972 standard; DNA; 555 BP.
XX
AC ABS21972;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID NO 21963.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagazer syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 4; SEQ ID NO 21963; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
```

mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCATCTCCGATTC 18
|||||
Db 424 GGCTCCATCTCCGATTC 441

RESULT 9

ACH73889
ID ACH73889 standard; DNA; 559 BP.

XX ACH73889;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #7084..

XX Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

XX (RANK/) RANK D R.

XX (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.

XX Claim 15; SEQ ID NO 7084; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above). The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterising
XX alternative splicing events, in detecting and characterising gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids,
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 559;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCATCTCCGATTC 18

Db 19 GGCTCCATCTCCGATTC 36

RESULT 10

ACH87595

ID ACH87595 standard; DNA; 564 BP.

XX ACH87595;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #20790.

XX Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human placenta.
 XX SQ
 PS Claim 25; SEQ ID NO 9498; 654pp; English.
 XX The present invention relates to single exon nucleic acid probes (SENP).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders
 CC SQ
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 600;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGCTCCCATCTCCGATTC 18
 |||||
 Db 443 GGCTCCCATCTCCGATTC 460

RESULT 13
 ABA28894
 ID ABA28894 standard; DNA; 600 BP.
 AC ABA28894;
 XX
 XX 23-JAN-2002 (first entry)
 DT
 DE Probe #7360 for gene expression analysis in human heart cell sample.
 XX Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 OS Homo sapiens.
 XX WO200157274-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000666.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 XX hearts.
 XX PT

PS Claim 1; SEQ ID NO 7360; 530pp; English.
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging,
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 600;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGCTCCCATCTCCGATTC 18
 |||||
 Db 443 GGCTCCCATCTCCGATTC 460

RESULT 14
 AAK35096
 ID AAK35096 standard; DNA; 600 BP.
 XX AAK35096;
 AC
 XX 06-NOV-2001 (first entry)
 DT
 DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
 XX Homo sapiens.
 OS
 XX WO200157276-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000668.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human bone marrow.
 XX Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention
 XX SQ
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18
|||||
Db 443 GGTCCTCATCTCCGATTC 460

RESULT 15

AAK09207
ID AAK09207 standard; DNA; 600 BP.
XX
AC AAK09207;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 9198.
XX
DE Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
(MOLE-) MOLECULAR DYNAMICS INC.

XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.

XX
PS Example 4; SEQ ID NO 9198; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention

XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18
|||||
Db 443 GGTCCTCATCTCCGATTC 460

Search completed: February 4, 2005, 21:52:43
Job time : 232.23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-9
Perfect score: 18
Sequence: 1 ggtctcatctccgattc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:

1: gb_est1.*
2: gb_est2.*
3: gb_htc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	243	4	BM409971 EST584298
2	18	100.0	279	2	AW247015 2822471.5
3	18	100.0	344	8	A2576742 AST-2T009
4	18	100.0	382	4	BM855440 K-EST0138
5	18	100.0	408	2	AW933481 EST359240
6	18	100.0	421	4	BM844286 K-EST0122
7	18	100.0	421	6	CF145335 UI-HF-CB0
8	18	100.0	453	2	AW930419 EST340792
9	18	100.0	455	1	AI777656 EST258451
10	18	100.0	474	7	CM422261 170004245
11	18	100.0	503	1	AI283063 qm62c06.x
12	18	100.0	503	4	BM857244 K-EST0141
13	18	100.0	542	7	CM422262 170004245
14	18	100.0	560	6	CD675630 fs25h07.Y
15	18	100.0	571	2	AW931273 EST357116
16	18	100.0	577	6	CF131978 UI-HF-FQ0
17	18	100.0	584	1	AL134785 DKEZps47K
18	18	100.0	587	2	AW931455 EST357298
19	18	100.0	587	2	BE871836 601447837
20	18	100.0	596	2	AW442063 EST311459
21	18	100.0	596	2	AW732926 bb17b09.Y
22	18	100.0	597	2	AW930783 EST356626
23	18	100.0	597	2	AW931219 EST357062
24	18	100.0	603	2	AW930433 EST340806

25	18	100.0	605	2	AW931446
c 26	18	100.0	606	7	CN422268
c 27	18	100.0	612	2	BE783664
c 28	18	100.0	614	2	BE206897
c 29	18	100.0	616	6	CF132307
c 30	18	100.0	624	6	CF131456
c 31	18	100.0	632	7	CN422264
c 32	18	100.0	635	4	BI489889
c 33	18	100.0	638	4	BI924992
c 34	18	100.0	657	2	BE207063
c 35	18	100.0	671	2	AW814739
c 36	18	100.0	688	4	BG708652
c 37	18	100.0	688	4	BM409531
c 38	18	100.0	697	4	BI457116
c 39	18	100.0	697	5	BU184922
c 40	18	100.0	700	4	BG831301
c 41	18	100.0	702	6	CF125275
c 42	18	100.0	704	4	BI561500
c 43	18	100.0	707	6	CD636467
c 44	18	100.0	711	2	BE535474
c 45	18	100.0	720	6	CD636470

ALIGNMENTS

RESULT 1

BM409971

LOCUS

EST584298

tomato breaker fruit lycopersicon esculentum cDNA clone

243 bp mRNA linear EST 22-JAN-2002

CLEGS0N22 5' end, mRNA sequence.

BM409971

GI:18261601

EST

Lycopersicon esculentum (tomato)

Lycopersicon esculentum

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 243)

Alcala, J., Vrebalov, J., White, R., Vision, T., Karanycheva, S.A., Tsai, J., Bongri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.

Generation of ESTs from tomato fruit tissue, breaker stage (2002)

Unpublished (2002)

Contact: CUGI

Clemson University

Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics Institute

Seq primer: T3.

Location/Qualifiers

1. 243

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clones="CLEGS0N22"

/tissue_type="Pericarp"

/dev stage="breaker"

/lab_host="SOLR"

/clone_lib="tomato breaker fruit"

/notes="Vector: pBluescriptSKMUCadapt; Site 1: EcoRI; Site 2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 243;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCATCTCCGATTC 18
 |||||
 Db 24 GGCTCCATCTCCGATTC 41

RESULT 2
 AW247015/c
 LOCUS
 DEFINITION 279 bp mRNA linear EST 07-JAN-2000
 2822471.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822471 5',
 mRNA sequence.

ACCESSION AW247015
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS 1 (bases 1 to 279)
 TITLE NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Other ESTs: 2822471.3prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-i@mail.nih.gov
 Tissue Procurement: DCTD/DTT cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (ILMI) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/ILMI at:
 www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite. Poly-r Identification: patMatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu
 Plate: LLCM9 row: H column: 24
 High quality sequence stop: 199.

FEATURES
 source
 1..279
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2822471"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_7"
 /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5',
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
 Query Match 100.0%; Score 18; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCATCTCCGATTC 18
 |||||
 Db 197 GGCTCCATCTCCGATTC 180

RESULT 3
 AZ576742

LOCUS
 DEFINITION 344 bp DNA linear GSS 06-DEC-2000
 AST-2T00919 Genetrap T47D Human Breast Carcinoma Library Homo
 sapiens genomic 5', genomic survey sequence.

ACCESSION AZ576742
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS 1 (bases 1 to 344)
 TITLE Exon-trap tags from a T47D GenomesScreen(TM) Library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Greg Henkel
 Gene Expression
 Aurora Biosciences Corp.
 11010 Torreyana Road, San Diego, CA 92121, USA
 Tel: 8584048436
 Fax: 8584046719
 Email: henkelg@aurorabio.com
 Pools of cells were isolated from a GenomesScreen(TM) library. The
 library of cells was generated by retroviral integration of a gene
 tagging element consisting of: 1) A promoterless beta-lactamase
 proceeded by a splice acceptor as a reporter for gene expression;
 2) A promoter driving neomycin resistance followed by a splice
 donor to trap downstream exons. 3' RACE from neomycin gene was
 performed using total RNA from isolated pools. Output was shotgun
 cloned in pAMP-1 and used to transform DH5-alpha competent
 bacteria. 5' ends of reported sequences were immediately preceded
 by splice donor from the trapping construct.
 Class: exon-trapped.

FEATURES
 source
 1..344
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /tissue_type="Carcinoma"
 /cell_type="Epithelial"
 /cell_line="T47D"
 /clone_lib="Genetrap T47D Human Breast Carcinoma Library"
 /note="Organ: Breast; Vector: pAMP-1; 3' RACE of total RNA
 from genetrap pools; shotgun clone in pAMP-1 and used to
 transform DH5-alpha competent bacteria."

ORIGIN
 Query Match 100.0%; Score 18; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCATCTCCGATTC 18
 |||||
 Db 303 GGCTCCATCTCCGATTC 320

RESULT 4
 BM855440/c
 LOCUS
 DEFINITION 382 bp mRNA linear EST 06-MAR-2002
 K-EST0138319 S21SNUS20 Homo sapiens cDNA clone S21SNUS20-67-G02 5',
 mRNA sequence.

ACCESSION BM855440
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS 1 (bases 1 to 382)
 TITLE 21C Frontier Korean EST Project 2001
 Kim, Y.S.
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Lee, J.H., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Kim, Y.S.

JOURNAL
COMMENT

Unpublished (2002)

Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 67 row: G column: 02
High quality sequence stop: 382.

FEATURES

source

```
1. 382
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNU520-67-G02"
/sex="F"
/tissue_type="Stomach"
/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_host="Top10F"
/clone_lib="S21SNU520"
/notes="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI. The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
```

ORIGIN

```
Query Match 100.0%; Score 18; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GGTCTCCATCTCCGATTC 18

|||||

Db 377 GGTCTCCATCTCCGATTC 360

RESULT 5

AW933481

LOCUS

```
DEFINITION EST359240 tomato fruit mature green, TAMU Lycopersicon esculentum
cDNA clone cLEF53L24 5', mRNA sequence.
```

ACCESSION

AW933481

VERSION

AW933481.1

KEYWORDS

EST.

SOURCE

Lycopersicon esculentum (tomato)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE

1 (bases 1 to 408)

Alcala, J., Vrebalov, J., White, R., Matern, A. L., Holt, I. E., Liang, F., Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., and

Ronnig, C. M., Fraser, C. M., Martin, G. B., Tanksley, S. D., and

Giovannoni, J.

Generation of ESTs from tomato fruit tissue

Unpublished (1999)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

FEATURES

source

```
1. 408
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEF53L24"
/tissue_type="fruit pericarp"
/dev stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
/clone_lib="tomato fruit mature green, TAMU"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLEF - Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the pericarp"
```

ORIGIN

```
Query Match 100.0%; Score 18; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GGTCTCCATCTCCGATTC 18

|||||

Db 67 GGTCTCCATCTCCGATTC 84

RESULT 6

BM844286/c

LOCUS

```
DEFINITION K-EST0123378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5',
mRNA sequence.
```

ACCESSION

BM844286

VERSION

BM844286.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 421)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 63 row: B column: 03

High quality sequence stop: 421.

Location/Qualifiers

1. 421

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S12SNU216-63-B03"

/sex="F"

/tissue_type="Lymph node"

/cell_type="Epithelial"

/cell_line="SNU-216"

/lab_host="Top10F"

/clone_lib="S12SNU216"

/notes="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18

Db 144 GGTCCTCATCTCCGATTC 127

RESULT 7

CF145335/c

LOCUS CF145335 421 bp mRNA linear EST 06-AUG-2003
DEFINITION UI-HF-CH0-asn-f-06-0-UI.r1 NIH_MGC_210 Homo sapiens cDNA clone
IMAGE:30569057 5', mRNA sequence.

ACCESSION CF145335

VERSION CF145335.1 GI:33260779

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 421)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 889548

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu

Tissue Procurement: Tim Ratliff
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/humanfl.html>

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers
1..421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30569057"
/tissue_type="CNCAP(3)/T-225 cell line"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_MGC_210"
/notes="Organ: Prostate; Vector: pT7T3 Pac; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dt
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned

directionally into pT7T3 Pac vector. The library tag
sequence located between the Not I site and the polyA tail
is CCCAC. Tissue was provided by Tim Ratliff."

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18

Db 138 GGTCCTCATCTCCGATTC 121

RESULT 8

AW930419

LOCUS AW930419

DEFINITION EST340792 tomato fruit mature green, TAMU Lycopersicon esculentum
CDNA clone CLEF42D3 5', mRNA sequence.

ACCESSION AW930419

VERSION AW930419.1 GI:8105736

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 453)

AUTHORS

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
Giovannoni,J.

TITLE Generation of ESTs from tomato fruit tissue

JOURNAL Unpublished (1999)

COMMENT Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

FEATURES

source

Location/Qualifiers
1..453
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEF42D3"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
/clone_lib="tomato fruit mature green, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; cLEF - Fruit were tagged at the 1cm stage and
harvested 3-5 days prior to ripening. Fruit were cut in
half to verify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
pericarp"

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18

Db 94 GGTCCTCATCTCCGATTC 111

RESULT 9

AI777656

LOCUS AI777656

DEFINITION EST258451 tomato susceptible, Cornell Lycopersicon esculentum cDNA
clone cLES2M16, mRNA sequence.

ACCESSION AI777656
 VERSION AI777656.1 GI:5275613
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 455)
 D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
 Liang, F., Upton, J., Romning, C.M., Craven, M.B., Fujii, C.Y.,
 Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
 Giovannoni, J.J., and Martin, G.B.
 Generation of ESTs from *Pseudomonas* susceptible tomato
 Contact: CUGI
 Unpublished (1999)
 TITLE Lycopersicon esculentum
 JOURNAL
 COMMENT

FEATURES

source
 1..455
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="R11-13 (Rio Grande x Money Maker)"
 /db_xref="taxon:4081"
 /clone="CL52M16"
 /tissue_type="leaf"
 /dev_stage="4-week old"
 /lab_host="SOUR"
 /clone_lib="tomato susceptible, Cornell"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; cLES - Tomato *Pseudomonas* Susceptible EST Library.
 Directionally cloned cDNAs inserted into pBluescript
 SK(-) at 5' end with EcoRI and 3' end with XhoI site"

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTCTCCATCTCCGATTC 18
 |||||
 Db 100 GGTCTCCATCTCCGATTC 117

RESULT 10
 CN422261/c
 LOCUS 17000424524125 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
 DEFINITION
 ACCESSION CN422261
 VERSION CN422261.1 GI:47409855
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 474)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, L.W.
 Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 JOURNAL
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 474 Std Error: 0.00.

FEATURES

source
 1..474
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, embryoid bodies
 derived from H1, H7 and H9 cells"
 /clone_lib="GRN_EB"
 /note="Oligo dT primed, full-length enriched cDNA library
 from embryoid body outgrowths derived from HES cell lines
 H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
 conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 474;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTCTCCATCTCCGATTC 18
 |||||
 Db 199 GGTCTCCATCTCCGATTC 182

RESULT 11

AI283063/c
 LOCUS qm52c06.x1 Soares placenta 8to9weeks 2NbHP8to9w Homo sapiens cDNA
 DEFINITION clone IMAGE:1893322 3' similar to SW:BCIX_HUMAN Q07817 APOPTOSIS
 REGULATOR BCL-X., mRNA sequence.
 ACCESSION AI283063
 VERSION AI283063.1 GI:3921296
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 503)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1323 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 440.

FEATURES

source
 1..503
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1893322"
 /dev_stage="two placentae: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares placenta 8to9weeks 2NbHP8to9w"
 /note="Organ: placenta; Vector: p773D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGAGCGCGCGATTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 503;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGTCCTCATCTCCGATTC 18
Db 494 GGTCCTCATCTCCGATTC 477

RESULT 12
BM857244/c
LOCUS BM857244 503 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0141477 S21SNUS20 Homo sapiens cDNA clone S21SNUS20-78-F09 5',
mRNA sequence.
ACCESSION BM857244
VERSION BM857244.1 GI:19213643
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yusong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 78 Row: F Column: 09
High quality sequence stop: 503.
FEATURES
source
1..503
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNUS20-78-F09"
/sex="F"
/tissue_types="Stomach"
/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_host="Top10F'"
/clone_lib="S21SNUS20"
/notes="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 503;
Best Local Similarity 100.0%; Pred. NO. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18
Db 145 GGTCCTCATCTCCGATTC 128

RESULT 13
CN422262/c
LOCUS CN422262 542 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424524143 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN422262
VERSION CN422262.1 GI:47409856
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 542)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 542 Std Error: 0.00.
FEATURES
source
1..542
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/notes="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN
Query Match 100.0%; Score 18; DB 7; Length 542;
Best Local Similarity 100.0%; Pred. NO. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18
Db 207 GGTCCTCATCTCCGATTC 190

RESULT 14
CD675630/c
LOCUS CD675630 560 bp mRNA linear EST 24-JUN-2003
DEFINITION fs2Sh07.y1 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone
fs2Sh07 5', mRNA sequence.
ACCESSION CD675630
VERSION CD675630.1 GI:32177361
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,
Bouffard,G., Smith,D. and Peterson,K.
TITLE Expressed sequence tag analysis of adult human lens for the NEIBank
Project: over 2000 non-redundant transcripts, novel genes and
splice variants
JOURNAL Mol. Vis. 8 (4), 171-184 (2002)
MEDLINE 22103463
PUBMED 12107413
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452

```

Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 25 row: h column: 07
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers

FEATURES

source

```
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fs25h07"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Lens CDNA (Normalized): fs"
/note="Organ: Eye; Vector: pCMVSPORT6; A human lens library (by) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."
```

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 560;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 GGTCTCCATCTCCGATTC 18
|||||
Db 370 GGTCTCCATCTCCGATTC 353
```

RESULT 15
 AW931273
 LOCUS AW931273 571 bp mRNA linear EST 18-MAY-2001
 DEFINITION EST357116 tomato fruit mature green, TAMU Lycopersicon esculentum
 CDNA clone CLEF44F15 5', mRNA sequence.
 AW931273
 ACCESSION AW931273
 VERSION AW931273.1 GI:8106674
 KEYWORDS EST

SOURCE
 Lycopersicon esculentum (tomato)
 Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 571)
 AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, J.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 TITLE Generation of ESTs from tomato fruit tissue
 JOURNAL Unpublished (1999)
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.
 Location/Qualifiers

```
1..571
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEF44F15"
/tissue_type="fruit pericarp"
```

FEATURES

source

```
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
/clone_lib="tomato fruit mature green, TAMU"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLEF - Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the pericarp"
```

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 571;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 GGTCTCCATCTCCGATTC 18
|||||
Db 104 GGTCTCCATCTCCGATTC 121
```

Search completed: February 5, 2005, 08:11:49
 Job time : 2147.2 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-10
Perfect score: 18
Sequence: 1 cctggggtgatgtggagc 18
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	6	BD235158
2	18	100.0	18	6	BD235177
3	18	100.0	391	4	AF245495
4	18	100.0	512	6	CQ272769
5	18	100.0	541	4	AF245487
6	18	100.0	541	4	AF245488
7	18	100.0	541	4	AF245489
8	18	100.0	555	6	CQ113695
9	18	100.0	555	6	CQ152574
10	18	100.0	555	6	CQ185831
11	18	100.0	555	6	CQ235904
12	18	100.0	555	6	CQ273477
13	18	100.0	555	6	CQ310858
14	18	100.0	555	6	CQ347773
15	18	100.0	600	6	CQ100639
16	18	100.0	600	6	CQ139631
17	18	100.0	600	6	CQ175964
18	18	100.0	600	6	CQ222999
19	18	100.0	600	6	CQ260961

20	18	100.0	600	6	CQ298444
21	18	100.0	600	6	CQ335104
22	18	100.0	636	6	BD097037
23	18	100.0	702	4	AY005131
24	18	100.0	702	4	BD084108
25	18	100.0	702	6	BD102202
26	18	100.0	702	9	BT007208
27	18	100.0	702	12	BT008248
28	18	100.0	720	4	AF216205
29	18	100.0	723	9	HSU72398
30	18	100.0	737	6	AR054022
31	18	100.0	737	6	AR172595
32	18	100.0	737	6	IS2012
33	18	100.0	737	6	AR371662
34	18	100.0	737	6	AR380913
35	18	100.0	737	9	HSBCLXS
36	18	100.0	747	6	AX127722
37	18	100.0	752	4	SSJ001203
38	18	100.0	766	4	AF164517
39	18	100.0	926	6	AR054021
40	18	100.0	926	6	AR118504
41	18	100.0	926	6	AR124952
42	18	100.0	926	6	AR144311
43	18	100.0	926	6	AR172594
44	18	100.0	926	6	BD243042
45	18	100.0	926	6	CQ765842

ALIGNMENTS

RESULT 1	BD235158	18 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD235158	18 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Oligonucleotide inhibitors of bcl-xL.				
ACCESSION	BD235158				
VERSION	JP 2002519048-A/10.				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Stein, C.A.				
TITLE	Oligonucleotide inhibitors of bcl-xL				
JOURNAL	Patent: JP 2002519048-A 10 02-JUL-2002;				
COMMENT	THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK				
	OS Artificial Sequence				
	PN JP 2002519048-A/10				
	PD 02-JUL-2002				
	PF 02-JUL-1999 JP 2000557839				
	PR 02-JUL-1998 US 09/109614				
	PI CY A STEIN				
	PC				
	C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC				
	A61K47/42,				
	PC A61K47/48 A61K48/00 A61P35/00,C12N15/00				
	CC ANTISENSE OLIGONUCLEOTIDE				
	PH Key Location/Qualifiers				
	FT source 1..18				
	FT Location/Qualifiers				
	1..18				
	/organism='Artificial Sequence'.				
	FEATURES				
	source				
	1..18				
	/organism='synthetic construct'				
	/mol_type='genomic DNA'				
	/db_xref='taxon:32630'				
	ORIGIN				
	Query Match 100.0%; Score 18; DB 6; Length 18;				
	Best Local Similarity 100.0%; Pred. No. 1.8e+02;				
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
	QY 1 CCTGGGGTGTATGTGGAGC 18				

AUTHORS Amills, M. and Bouzat, J.
 TITLE Characterization of the bovine bcl-xL gene and related pseudogenes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 541)
 AUTHORS Amills, M. and Bouzat, J.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain

FEATURES
 source
 1..541
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="1.1"
 <1..>541
 /codon_start=1
 /product="anti-apoptotic regulator Bcl-xL"
 /protein_id="AAK31306.1"
 /db_xref="GI:13591636"
 /translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG
 DEFELRYRAFSDLTSLQHTPGTAYQSFQVNVNLFPRDGVNWRIVAFSPFGALCV
 ESDVKEMQVLVSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKQERF
 NRWFLTGMTVAGVVLGSLF"

ORIGIN
 Query Match 100.0%; Score 18; DB 4; Length 541;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18
 |||||
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 6
 AF245488/c
 LOCUS Bos taurus clone 1.2 anti-apoptotic regulator Bcl-xL mRNA, partial cds.
 DEFINITION
 ACCESSION AF245488.1 GI:13591637
 VERSION
 KEYWORDS
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 541)
 AUTHORS Amills, M. and Bouzat, J.
 TITLE Characterization of the bovine bcl-xL gene and related pseudogenes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 541)
 AUTHORS Amills, M. and Bouzat, J.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain

FEATURES
 source
 1..541
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="1.2"
 <1..>541
 /codon_start=1
 /product="anti-apoptotic regulator Bcl-xL"
 /protein_id="AAK31307.1"
 /db_xref="GI:13591638"
 /translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG
 DEFELRYRAFSDLTSLQHTPGTAYQSFQVNVNLFPRDGVNWRIVAFSPFGALCV
 ESDVKEMQVLVSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKQERF
 NRWFLTGMTVAGVVLGSLF"

ORIGIN
 Query Match 100.0%; Score 18; DB 4; Length 541;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18
 |||||
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 7
 AF245489/c
 LOCUS Bos taurus clone 1.3 anti-apoptotic regulator Bcl-xL mRNA, partial cds.
 DEFINITION
 ACCESSION AF245489.1 GI:13591639
 VERSION
 KEYWORDS
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 541)
 AUTHORS Amills, M. and Bouzat, J.
 TITLE Characterization of the bovine bcl-xL gene and related pseudogenes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 541)
 AUTHORS Amills, M. and Bouzat, J.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain

FEATURES
 source
 1..541
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="1.3"
 <1..>541
 /codon_start=1
 /product="anti-apoptotic regulator Bcl-xL"
 /protein_id="AAK31308.1"
 /db_xref="GI:13591640"
 /translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG
 DEFELRYRAFSDLTSLQHTPGTAYQSFQVNVNLFPRDGVNWRIVAFSPFGALCV
 ESDVKEMQVLVSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKQERF
 NRWFLTGMTVAGVVLGSLF"

ORIGIN
 Query Match 100.0%; Score 18; DB 4; Length 541;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18
 |||||
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 8
 CQ113695
 LOCUS Sequence 22554 from Patent WO0157272.
 DEFINITION
 ACCESSION CQ113695
 VERSION CQ113695.1 GI:41083565
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

ORIGIN
 Query Match 100.0%; Score 18; DB 4; Length 541;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18
 |||||
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 7
 AF245489/c
 LOCUS Bos taurus clone 1.3 anti-apoptotic regulator Bcl-xL mRNA, partial cds.
 DEFINITION
 ACCESSION AF245489.1 GI:13591639
 VERSION
 KEYWORDS
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 541)
 AUTHORS Amills, M. and Bouzat, J.
 TITLE Characterization of the bovine bcl-xL gene and related pseudogenes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 541)
 AUTHORS Amills, M. and Bouzat, J.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain

FEATURES
 source
 1..541
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="1.3"
 <1..>541
 /codon_start=1
 /product="anti-apoptotic regulator Bcl-xL"
 /protein_id="AAK31308.1"
 /db_xref="GI:13591640"
 /translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG
 DEFELRYRAFSDLTSLQHTPGTAYQSFQVNVNLFPRDGVNWRIVAFSPFGALCV
 ESDVKEMQVLVSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKQERF
 NRWFLTGMTVAGVVLGSLF"

ORIGIN
 Query Match 100.0%; Score 18; DB 4; Length 541;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18
 |||||
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 8
 CQ113695
 LOCUS Sequence 22554 from Patent WO0157272.
 DEFINITION
 ACCESSION CQ113695
 VERSION CQ113695.1 GI:41083565
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

```

TITLE      Human genome-derived single exon nucleic acid probes useful for
JOURNAL    analysis of gene expression in human placenta
            Patent: WO 0157272-A 22554 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9~EXPRESSED IN PLACENTA, SIGNAL =
            0.99~SWISSPROT HIT: Q07817, EVALUATE 1.00e-106~EST HUMAN
            HIT: BE207063.1, EVALUATE 0.00e+00~NT HIT: U72398.1, EVALUATE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 9
CQ152574
LOCUS      CQ152574      555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION      Sequence 22596 from Patent WO0157276.
ACCESSION      CQ152574
VERSION      CQ152574.1 GI:41159924
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human bone marrow
JOURNAL      Patent: WO 0157276-A 22596 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9~EXPRESSED IN BONE MARROW, SIGNAL
            = 4.7~SWISSPROT HIT: Q07817, EVALUATE 1.00e-106~EST HUMAN
            HIT: BE207063.1, EVALUATE 0.00e+00~NT HIT: U72398.1, EVALUATE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 10
CQ185831
LOCUS      CQ185831      555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION      Sequence 17227 from Patent WO0157274.
ACCESSION      CQ185831
VERSION      CQ185831.1 GI:41180846
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1

```

```

AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human heart
JOURNAL      Patent: WO 0157274-A 17227 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9~EXPRESSED IN HEART, SIGNAL =
            1.4~SWISSPROT HIT: Q07817, EVALUATE 1.00e-106~EST HUMAN HIT:
            BE207063.1, EVALUATE 0.00e+00~NT HIT: U72398.1, EVALUATE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 11
CQ235904
LOCUS      CQ235904      555 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION      Sequence 22743 from Patent WO0157273.
ACCESSION      CQ235904
VERSION      CQ235904.1 GI:41219182
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
            ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
            3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
            60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
            August 2000 (03.08.00)<150> GB 24263,6<151> 03 October 2000
            (03.10.00)<150> US 60/236,359<151> 27 September 2000
            (27.09.00)<150> US 60/234,687<151> 21 September 2000
            (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
            Molecular Dynamics Sequence Listing Engine
JOURNAL      Patent: WO 0157273-A 22743 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9~EXPRESSED IN ADULT LIVER, SIGNAL
            = 1.7~SWISSPROT HIT: Q07817, EVALUATE 1.00e-106~EST HUMAN
            HIT: BE207063.1, EVALUATE 0.00e+00~NT HIT: U72398.1, EVALUATE
            0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 12
CQ273477
LOCUS      CQ273477      555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION      Sequence 21738 from Patent WO0157277.

```

```
ACCESSION      CQ273477
VERSION        CQ273477.1  GI:41246081
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL       Patent: WO 0157277-A 21738 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..555
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
              = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
              HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
              0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 13
CQ310858
LOCUS      CQ310858          555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21963 from Patent WO0186003.
ACCESSION  CQ310858
VERSION    CQ310858.1  GI:41271435
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human lung
JOURNAL   Patent: WO 0186003-A 21963 15-NOV-2001;
          Aeomica, Inc. (US)
FEATURES  Location/Qualifiers
          source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
          2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
          BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
          0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 14
CQ347773
LOCUS      CQ347773          555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21963 from Patent WO0186003.
ACCESSION  CQ310858
VERSION    CQ310858.1  GI:41271435
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human lung
JOURNAL   Patent: WO 0186003-A 21963 15-NOV-2001;
          Aeomica, Inc. (US)
FEATURES  Location/Qualifiers
          source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
          2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
          BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
          0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

DEFINITION Sequence 21867 from Patent WO0157275.
ACCESSION  CQ347773
VERSION    CQ347773.1  GI:41296844
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human brain
JOURNAL   Patent: WO 0157275-A 21867 09-AUG-2001;
          Aeomica, Inc. (US)
FEATURES  Location/Qualifiers
              source
                1..555
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
              1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
              BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
              0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 15
CQ100639
LOCUS      CQ100639          600 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 9498 from Patent WO0157272.
ACCESSION  CQ100639
VERSION    CQ100639.1  GI:41069665
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human placenta
JOURNAL   Patent: WO 0157272-A 9498 09-AUG-2001;
          Aeomica, Inc. (US)
FEATURES  Location/Qualifiers
              source
                1..600
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
              0.99"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      234 CCTGGGGTGATGTGGAGC 251

Search completed: February 4, 2005, 23:30:41
Job time : 432.664 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169a-10

Perfect score: 18

Sequence: 1 cctgggggtgatgtggagc 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_23Sep04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	Az46980 Bcl-X1 MR
2	18	100.0	555	4	Aba73433 Human foe
3	18	100.0	555	4	Aa153868 Probe #22
4	18	100.0	555	4	Aba38761 Probe #17
5	18	100.0	555	4	Aak48039 Human bon
6	18	100.0	555	4	Aak21876 Human bra
7	18	100.0	555	4	Abs47753 Human liv
8	18	100.0	555	4	Abs21972 Human gen
9	18	100.0	564	12	Ach87595 Human gen
10	18	100.0	600	4	Aba60917 Human foe
11	18	100.0	600	4	Aa140812 Probe #94
12	18	100.0	600	4	Aba28894 Probe #73
13	18	100.0	600	4	Aak35096 Human bon
14	18	100.0	600	4	Aak09207 Human bra
15	18	100.0	600	4	Abs34848 Human liv
16	18	100.0	600	6	Abs09558 Human gen
17	18	100.0	636	4	Aah48169 Mutant bc
18	18	100.0	702	5	Aah43464 cDNA clon
19	18	100.0	702	12	Adm45994 Human apo
20	18	100.0	737	2	Aa81699 Human thy
21	18	100.0	737	10	Abz83507 Toxicolog

c	22	18	100.0	737	11	ADI32132	Adi32132 Human CDN
c	23	18	100.0	739	12	ADG65218	Adg65218 Human Bcl
c	24	18	100.0	747	4	AAF30926	Aaf30926 Human Bcl
c	25	18	100.0	747	12	ADG65209	Adg65209 Human Bcl
c	26	18	100.0	926	2	AAQ81698	Aaq81698 Human thy
c	27	18	100.0	926	2	AA740079	Aat40079 Bcl-XL ge
c	28	18	100.0	926	3	AAZ93614	Aaz93614 Bcl-x gen
c	29	18	100.0	926	4	AA515189	Aas15189 Human bcl
c	30	18	100.0	926	4	AAAC90810	Aac90810 Human Bcl
c	31	18	100.0	926	6	ABK84766	Abk84766 Human CDN
c	32	18	100.0	926	8	ABT16641	Abt16641 Human bcl
c	33	18	100.0	926	10	ADD56779	Add56779 Human bcl
c	34	18	100.0	926	10	AA64187	Aad4187 Human bcl
c	35	18	100.0	926	11	ADI32104	Adi32104 Human CDN
c	36	18	100.0	926	12	ADH52630	Adh52630 Human ant
c	37	18	100.0	926	12	ADQ19990	Ado19990 Human PRO
c	38	18	100.0	926	12	ADP13351	Adp13351 Renal cel
c	39	18	100.0	1216	5	AAS00247	Aas00247 Bcl-X1-DT
c	40	18	100.0	1455	5	AAS00250	Aas00250 LFn-Bcl-X
c	41	18	100.0	2386	10	ADG89403	Adg89403 Cancer de
c	42	18	100.0	2386	12	ADN04260	Adn04260 Antipsori
c	43	18	100.0	2575	12	ADQ19866	Ado19866 Human PRO
c	44	18	100.0	7372	2	AAX33182	Aax33182 Base sequ
c	45	16.4	91.1	492	9	ACH46093	Ach46093 Human inf

ALIGNMENTS

RESULT 1

AAZ46980

ID AAZ46980 standard; DNA; 18 BP.

XX

AC AAZ46980;

DT 14-APR-2000 (first entry)

XX Bcl-X1 mRNA specific antisense oligo J.

DE Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;

KW lung; bladder; bcl-2; vascular lesion; antisense; ss.

XX Homo sapiens.

OS WO200001393-A2.

PN 13-JAN-2000.

XX 02-JUL-1999; 99WO-US015250.

XX 02-JUL-1998; 98US-00109614.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Stein CA;

XX WPI; 2000-137140/12.

XX New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English.

XX The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
 CC represent antisense oligos specific for the bcl-X1 mRNA

XX Sequence 18 BP; 2 A; 3 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
 Db 1 CCTGGGGTGATGTGGAGC 18

RESULT 2
 ABA73433
 ID ABA73433 standard; DNA; 555 BP.

XX AC ABA73433;
 XX DT 01-FEB-2002 (first entry)
 XX DE Human foetal liver single exon nucleic acid probe #21738.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX OS Homo sapiens.
 XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PS WPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 gene expression in human fetal liver.

XX PS Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring
 human gene expression in a sample derived from human foetal liver. The
 single exon nucleic acid probes may be used for predicting, measuring and
 displaying gene expression in samples derived from human fetal liver. The
 present sequence is a single exon nucleic acid probe of the invention.
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
 Db 215 CCTGGGGTGATGTGGAGC 232

RESULT 3
 AAI53868
 ID AAI53868 standard; DNA; 555 BP.

XX AC AAI53868;

XX DT 17-OCT-2001 (first entry)

XX DE Probe #22554 used to measure gene expression in human placenta sample.

XX KW Probe; microarray; human; placenta; antenatal diagnosis;
 genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PS WPI; 2001-488897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 gene expression in human placenta.

XX PS Claim 25; SEQ ID NO 22554; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP).
 The present sequence is one such probe. The probes are useful for
 producing a microarray for predicting, measuring and displaying gene
 expression in samples derived from human placenta. The probes are useful
 for antenatal diagnosis of human genetic disorders

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
 Db 215 CCTGGGGTGATGTGGAGC 232

RESULT 4
 ABA38761
 ID ABA38761 standard; DNA; 555 BP.

XX AC ABA38761;

XX DT 23-JAN-2002 (first entry)

XX DE Probe #17227 for gene expression analysis in human heart cell sample.

XX KW Human; gene expression; heart; microarray; vascular system; probe;
 cardiovascular disease; hypertension; cardiac arrhythmia;

XX KW congenital heart disease; ss.


```
OS Homo sapiens.
XX WO200157274-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000666.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX Claim 4; SEQ ID NO 17227; 530pp; English.
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 4; Length 555;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCTGGGGTGATGTGGAGC 18
XX |||||
XX Db 215 CCTGGGGTGATGTGGAGC 232
XX
XX RESULT 5
XX AAK48039
XX ID AAK48039 standard; DNA; 555 BP.
XX AC AAK48039;
XX AC
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 22596.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Query Match 100.0%; Score 18; DB 4; Length 555;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCTGGGGTGATGTGGAGC 18
XX |||||
XX Db 215 CCTGGGGTGATGTGGAGC 232
XX
XX RESULT 6
XX AAK21876
XX ID AAK21876 standard; DNA; 555 BP.
XX AC AAK21876;
XX AC
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 21867.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX KW ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Query Match 100.0%; Score 18; DB 4; Length 555;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCTGGGGTGATGTGGAGC 18
XX |||||
XX Db 215 CCTGGGGTGATGTGGAGC 232
XX
XX RESULT 6
XX AAK21876
XX ID AAK21876 standard; DNA; 555 BP.
XX AC AAK21876;
XX AC
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 21867.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX KW ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
```

```
XX PS Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGGGTGATGTGGAGC 18
Db 215 CCTGGGGTGATGTGGAGC 232
RESULT 7
ID ABS47753 standard; DNA; 555 BP.
XX AC ABS47753;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver single exon probe, SEQ ID No 22743.
XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
XX KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
XX KW coronary heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human adult liver.
XX PS Claim 4; SEQ ID NO 22743; 658pp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/ fragments). The probe hybridises at high
XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX CC (I) may be used for predicting, measuring and displaying gene expression
XX CC in samples derived from human adult liver. The genes identified may be
XX CC involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX CC associated with coronary heart disease. ABS25011-ABS51005 represent human
```

```
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification and was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGGGTGATGTGGAGC 18
Db 215 CCTGGGGTGATGTGGAGC 232
RESULT 8
ID ABS21972 standard; DNA; 555 BP.
XX AC ABS21972;
XX DT 19-AUG-2002 (first entry)
XX DE Human genome-derived single exon probe ORF from lung SEQ ID No 21963.
XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW primary ciliary dyskinesia; pulmonary hypertension;
XX KW hyaline membrane disease; open reading frame; ORF.
XX OS Homo sapiens.
XX PN WO200186003-A2.
XX PD 15-NOV-2001.
XX PF 30-JAN-2001; 2001WO-US0000665.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX PT Spatially-addressable set of single exon nucleic acid probes, used to
XX PT measure gene expression in human lung samples.
XX PS Claim 4; SEQ ID NO 21963; 634pp; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human lung comprising single exon nucleic acid probes having one of
XX CC 12614 nucleic acid sequences mentioned in the specification, or their
XX CC complements or the 12387 open reading frames derived from the 12614
XX CC probes. Also included are a microarray comprising the novel set of probes
XX CC ; the novel set of probes which hybridise at high stringency to a nucleic
XX CC acid expressed in the human lung; measuring gene expression in a sample
XX CC derived from human lung, comprising (a) contacting the array with a
XX CC collection of detectably labeled nucleic acids derived from human lung
```

mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 555;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGTGTGGAGC 18

Db 215 CCTGGGGTGTGTGGAGC 232

RESULT 9

ACH87595

ID ACH87595 standard; DNA; 564 BP.

XX

AC ACH87595;

XX

DT 29-JUL-2004 (first entry)

XX

XX Human genome derived single exon probe #20790.

DE

KW Human; probe; ss; gene expression; single exon probe; microarray;

KW alternative splicing event; genomic alteration.

XX

OS Homo sapiens.

XX

XX US2003194704-A1.

XX

PD 16-OCT-2003.

XX

XX 03-APR-2002; 2002US-00029386.

PF

XX 03-APR-2002; 2002US-00029386.

PR

XX (PENN/) PENN S G.

XX

FA (RANK/) RANK D R.

XX

FA (HANKZ/) HANKZ D K.

XX

PI Penn SG, Rank DR, Hanzel DK;

XX

XX WPI; 2004-119264/12.

DR

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX

PS Claim 1; SEQ ID NO 20790; 80pp; English.

XX

CC The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above). The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 564;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGTGTGGAGC 18

Db 215 CCTGGGGTGTGTGGAGC 232

RESULT 10

ABAG0917

ID ABAG0917 standard; DNA; 600 BP.

XX

AC ABAG0917;

XX

DT 01-FEB-2002 (first entry)

DE

XX Human foetal liver single exon nucleic acid probe #9222.

XX

KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX

OS Homo sapiens.

XX

XX WO200157277-A2.

XX

XX 09-AUG-2001.

XX

XX 30-JAN-2001; 2001WO-US000669.

PF

XX 04-FEB-2000; 2000US-0180312P.

PR

PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 DR
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 PT
 XX Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.
 PS
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 600;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTGGGGTGATGTGGAGC 18
 Db 234 CCTGGGGTGATGTGGAGC 251
 RESULT 11
 AAI40812
 ID AAI40812 standard; DNA; 600 BP.
 AC AAI40812;
 XX
 DT 17-OCT-2001 (first entry)
 DE Probe #9498 used to measure gene expression in human placenta sample.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000663.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 DR
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 PT
 XX Claim 1; SEQ ID NO 7360; 530pp; English.
 PS
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging, the
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX
 PS Claim 25; SEQ ID NO 9498; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENPs).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders
 XX
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 600;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTGGGGTGATGTGGAGC 18
 Db 234 CCTGGGGTGATGTGGAGC 251
 RESULT 12
 ABA28894
 ID ABA28894 standard; DNA; 600 BP.
 XX
 AC ABA28894;
 XX
 DT 23-JAN-2002 (first entry)
 DE Probe #7360 for gene expression analysis in human heart cell sample.
 XX
 KW Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157274-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000666.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 DR
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 PT
 XX Claim 1; SEQ ID NO 7360; 530pp; English.
 PS
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging, the
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic

CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
 XX Query Match 100.0%; Score 18; DB 4; Length 600;
 XX Best Local Similarity 100.0%; Pred. No. 65;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
 |||||
 Db 234 CCTGGGGTGATGTGGAGC 251

RESULT 13

AAK35096
 ID AAK35096 standard; DNA; 600 BP.

XX AC AAK35096;

XX DT 06-NOV-2001 (first entry)

XX DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.

XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000668.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
 XX probes which are derived from genomic sequences expressed in the human
 XX bone marrow. They can be used to measure gene expression in bone marrow
 XX samples, which may enable the improved diagnosis and treatment of cancers
 XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
 XX the probes of the invention

XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 4; Length 600;
 XX Best Local Similarity 100.0%; Pred. No. 65;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
 |||||
 Db 234 CCTGGGGTGATGTGGAGC 251

RESULT 14

AAK09207

ID AAK09207 standard; DNA; 600 BP.

XX AC AAK09207;

XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe SEQ ID NO: 9198.

XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KW ss.

XX OS Homo sapiens.

XX PN WO200157275-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000667.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human
 XX brains.

XX Example 4; SEQ ID NO 9198; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
 XX probes which are derived from genomic sequences expressed in the human
 XX brain. They can be used to measure gene expression in brain cell samples,
 XX which may enable the diagnosis and improved treatment of nervous system
 XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 XX epilepsy and cancers. The present sequence is one of the probes of the
 XX invention

XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 4; Length 600;
 XX Best Local Similarity 100.0%; Pred. No. 65;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
 |||||

Db 234 CCTGGGGTGATGTGGAGC 251
 |||||

RESULT 15

ABS34848

ID ABS34848 standard; DNA; 600 BP.

XX AC ABS34848;

XX DT 25-FEB-2003 (first entry)

XX DE Human liver single exon probe, SEQ ID No 9838.

XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 KW coronary heart disease; ss.

XX OS Homo sapiens.

```
XX WO200157273-A2.
XX
XX
XX PD
XX PF
XX PF
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX PR
XX 26-MAY-2000; 2000US-0207456P.
XX PR
XX 30-JUN-2000; 2000US-00608408.
XX PR
XX 03-AUG-2000; 2000US-00632366.
XX PR
XX 21-SEP-2000; 2000US-0234687P.
XX PR
XX 27-SEP-2000; 2000US-0236359P.
XX PR
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX DR WPI; 2001-488898/53.
XX
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human adult liver.
XX
XX PS Claim 1; SEQ ID NO 9838; 658pp; English.
XX
XX CC The invention relates to a single exon nucleic acid probe (SEN) (I) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification for complements/ fragments). The probe hybridises at high
XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX CC (I) may be used for predicting, measuring and displaying gene expression
XX CC in samples derived from human adult liver. The genes identified may be
XX CC involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX CC associated with coronary heart disease. ABS25011-ABS51005 represent human
XX CC liver single exon nucleic acid probes of the invention. Note: The
XX CC sequence information for this patent does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGAGC 18
Db 234 CCTGGGGTGATGTGAGC 251

Search completed: February 4, 2005, 21:52:43
Job time : 232.23 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169a-10
Perfect score: 18
Sequence: 1 cctgggggtgatgtggagc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	161	2 BE771987	BE771987 CM3-FT010
2	18	100.0	294	2 BE818722	BE818722 PM3-BN030
3	18	100.0	299	7 F08773	F08773 HSC25B061 n
4	18	100.0	305	4 B1399503	B1399503 MI-P-AV1
5	18	100.0	310	4 B1060608	B1060608 IL3-UT011
6	18	100.0	344	8 A2576742	A2576742 AST-2T009
7	18	100.0	418	4 B1051278	B1051278 CM3-GN029
8	18	100.0	421	4 BM844286	BM844286 K-EST0122
9	18	100.0	421	6 CF145335	CF145335 UI-HF-CB0
10	18	100.0	437	7 W01420	W01420 za73d06.r1
11	18	100.0	456	8 A2537061	A2537061 AST-2P015
12	18	100.0	474	7 CN422261	CN422261 170004245
13	18	100.0	475	5 BQ331598	BQ331598 MR4-ET013
14	18	100.0	478	4 BM050133	BM050133 6036332480
15	18	100.0	485	2 AW814883	AW814883 MR1-ST020
16	18	100.0	503	4 BM857244	BM857244 K-EST0141
17	18	100.0	516	7 H09884	H09884 ym05b07.r1
18	18	100.0	542	7 CN422262	CN422262 170004245
19	18	100.0	577	6 CF131978	CF131978 UI-HF-FQ0
20	18	100.0	584	1 AL134785	AL134785 DKFZP547K
21	18	100.0	587	2 BE871836	BE871836 601447837
22	18	100.0	608	4 B1960951	B1960951 MONOL_3A
23	18	100.0	611	6 CB448211	CB448211 702275 MA
24	18	100.0	612	2 BE783664	BE783664 601471247

c	25	18	100.0	632	7	CN422264	CN422264 170005326
c	26	18	100.0	657	2	BE207063	BE207063 ba09f05.Y
c	27	18	100.0	671	2	AW814739	AW814739 MR1-ST020
c	28	18	100.0	675	7	CK832794	CK832794 4056483 B
c	29	18	100.0	687	2	BE293685	BE293685 601186941
c	30	18	100.0	698	4	EG708652	EG708652 602673575
c	31	18	100.0	697	4	B1457116	B1457116 603183360
c	32	18	100.0	699	2	BE870269	BE870269 601447403
c	33	18	100.0	700	4	EG831301	EG831301 602766132
c	34	18	100.0	704	4	B1561500	B1561500 603256193
c	35	18	100.0	705	4	BG290422	BG290422 602388270
c	36	18	100.0	707	6	CD636467	CD636467 56049107H
c	37	18	100.0	714	4	EG470667	EG470667 602511594
c	38	18	100.0	716	7	CK317449	CK317449 SB02021A2
c	39	18	100.0	720	6	CD636470	CD636470 56049223J
c	40	18	100.0	735	6	CD641746	CD641746 AGENCOURT
c	41	18	100.0	765	2	BF569393	BF569393 602185659
c	42	18	100.0	782	2	BE249973	BE249973 600943141
c	43	18	100.0	798	5	BQ687097	BQ687097 AGENCOURT
c	44	18	100.0	798	5	BUS28551	BUS28551 AGENCOURT
c	45	18	100.0	798	7	CK000319	CK000319 AGENCOURT

ALIGNMENTS

RESULT 1
BE771987
LOCUS BE771987 161 bp mRNA linear EST 20-SEP-2000
DEFINITION CM3-FT0100-140700-245-e05 FT0100 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE771987
VERSION BE771987.1 GI:10225645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=CM3-FT0100-140700-245-e05&t3=2000-07-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 69.
Location/Qualifiers
1. 161
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0100"
/notes="Organ: prostate tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18
|||||
Db 107 CCTGGGGTGATGTGGAGC 124

RESULT 2

BE818722/c
LOCUS BE818722 294 bp mRNA linear EST 21-SEP-2000
DEFINITION PM3-BN0300-080700-002-g11 BN0300 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE818722
VERSION BE818722.1 GI:10250956
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM3-BN0300-080700-002-g11&t3=2000-07-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 33
High quality sequence stop: 294.

FEATURES

source
1..294
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0300"
/notes="Organ: breast normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18
|||||
Db 190 CCTGGGGTGATGTGGAGC 173

RESULT 3

F08773/c
LOCUS F08773 299 bp mRNA linear EST 20-FEB-1995
DEFINITION HSC25B061 normalized infant brain cDNA Homo sapiens cDNA clone c-25b06, mRNA sequence.
ACCESSION F08773
VERSION F08773.1 GI:673075
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS
1 (bases 1 to 299)
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M. D., Duprat, S., Houlgatte, R., Jumeau, M. N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
7757816
Contact: Genethon
GenexPress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169478600
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.

GenexPress library idt: C; Genexpress_sequence_idt: y3c-25b06
Seq primer: (-21)M13 universal.

FEATURES

source
1..299
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c-25b06"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/clone_lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII; Site 2: NotI; sex=Female; dev stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Souares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"

ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18
|||||
Db 71 CCTGGGGTGATGTGGAGC 54

RESULT 4

BI399503
LOCUS BI399503 305 bp mRNA linear EST 14-AUG-2001
DEFINITION MI-P-AVI-nrq-c-08-0-UI.s1 MI-P-AVI Sus scrofa cDNA clone MI-P-AVI-nrq-c-08-0-UI 3', mRNA sequence.
ACCESSION BI399503
VERSION BI399503.1 GI:15178564


```

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 305)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
889548
Contact: Tugle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: ctugle@iastate.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa Clone Distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=No.

Location/Qualifiers
1..305
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clones="MI-P-A11-nrg-c-08-0-UI"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="MI-P-A11"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-A11
library is normalized library derived from the MI-P-A10
library, ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.iastate.edu/. The procedure used to
create this library has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)
TAG_SEQ=None found"

Query Match 100.0%; Score 18; DB 4; Length 305;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
| | | | | | | | | | | | | | | | | |
Db 215 CCTGGGGTGATGTGGAGC 232

RESULT 5
BI060608
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BI060608 310 bp mRNA linear EST 15-JUN-2001
DEFINITION
IL3-UT0115-300101-433-B03 UT0115 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BI060608
VERSION
BI060608.1 GI:14468135
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 310)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20203663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0115-
300101-433-B03&t3=2001-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 310.

Location/Qualifiers
1..310
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0115"
/notes="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match 100.0%; Score 18; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
| | | | | | | | | | | | | | | | | |
Db 94 CCTGGGGTGATGTGGAGC 111

RESULT 6
AZ576742
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ576742 344 bp DNA linear GSS 06-DEC-2000
DEFINITION
AST-2T00919 Genetrap T47D Human Breast Carcinoma Library Homo
sapiens genomic 5', genomic survey sequence.
ACCESSION
AZ576742
VERSION
AZ576742.1 GI:11563053
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344)
Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M.,
Bernardino,A., Durick,K. and Pollok,B.
Exon-trap tags from a T47D GenomeScreen(TM) Library
Unpublished (2000)
Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkel@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase

```

proceeded by a splice acceptor as a reporter for gene expression;
 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAMP-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.

Class: exon-trapped.

FEATURES

Location/Qualifiers
 1..344

/organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /tissue_type="Carcinoma"
 /cell_type="Epithelial"
 /cell_line="T47D"

/clone_lib="Genetrap T47D Human Breast Carcinoma Library"
 /note="Organ: Breast; Vector: pAMP-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAMP-1 and used to transform DH5-alpha competent bacteria."

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18
 |||||
 Db 97 CCTGGGGTGATGTGGAGC 114

RESULT 7

BI051278

LOCUS

DEFINITION CM3-GN0297-110101-607-f03 GN0297 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI051278

VERSION BI051278.1

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 418)
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-110101-607-f03&t3=2001-01-11&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 3

High quality sequence stop: 418.

FEATURES

source

1..418
 /organism="Homo sapiens"
 /mol_type="mRNA"

/db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="GN0297"

/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 418;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18
 |||||
 Db 375 CCTGGGGTGATGTGGAGC 392

RESULT 8

BM844286/c

LOCUS

DEFINITION K-EST0122378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5', mRNA sequence.

ACCESSION BM844286

VERSION BM844286.1

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 421)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE

21C Frontier Korean EST Project 2001

JOURNAL

COMMENT

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 63 row: B column: 03

High quality sequence stop: 421.

location/Qualifiers

1..421

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S12SNU216-63-B03"

/sex="F"

/tissue_type="Lymph node"

/cell_type="Epithelial"

/cell_line="SNU-216"

/lab_host="Top10P"

/clone_lib="S12SNU216"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10⁺ by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
|||||
Db 353 CCTGGGGTGATGTGGAGC 336

RESULT 9

CFI45335/c

LOCUS

DEFINITION UI-HF-CBO-asn-f-06-0-UI-rl NIH_MGC_210 Homo sapiens cDNA clone
IMAGE:30569057 5', mRNA sequence.

ACCESSION CFI45335

VERSION CFI45335.1

KEYWORDS GI:33260779

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 421)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery

MEDLINE 97044477

PUBMED 8889548

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Tim Ratliff

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/humanfl.html

Seq primer: pyx-5.

Location/Qualifiers

FEATURES

source

1. .421

/organism="Homo sapiens"

/mol type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30569057"

/tissue_type="CNCAP(3)T-225 cell line"

/lab host="DH10B (T1 phage resistant)"

/clone lib="NIH_MGC_210"

/note="Organ: Prostate; Vector: pT7T3 Pac; Site 1: EcoR I;

Site 2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dr

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction. ligated

with EcoR I adaptor, digested with Not I and then cloned

directionally into pT7T3 Pac vector. The library tag

sequence located between the Not I site and the polyA tail

is CCCAC. Tissue was provided by Tim Ratliff."

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 18; DB 6; Length 421;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
|||||
Db 347 CCTGGGGTGATGTGGAGC 330

RESULT 10

W01420/c

LOCUS

DEFINITION

W01420 437 bp mRNA linear EST 18-APR-1996
za73d06.r1 Soares fetal lung NbHL19w Homo sapiens cDNA clone
IMAGE:298187 5', similar to SW:BCIX_HUMAN Q07817 APOPTOSIS REGULATOR

BCL-X, mRNA sequence.

ACCESSION W01420

VERSION W01420.1

KEYWORDS GI:1273428

SOURCE EST.

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 437)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and

Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.REGA-RT

High quality sequence stop: 383.

Location/Qualifiers

1. .437

/organism="Homo sapiens"

/mol type="mRNA"

/db_xref="GDB:1243109"

/db_xref="taxon:9606"

/clone="IMAGE:298187"

/dev stage="19 weeks"

/lab host="DH10B (ampicillin resistant)"

/clone lib="Soares fetal lung NbHL19w"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGAGCGCCGCAATTTTTTTTTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. This library was constructed

from the same fetus as the fetal heart library, Soares

fetal heart NbHL19w."

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 18; DB 7; Length 437;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
|||||

Db 106 CCTGGGGTGATGTGGAGC 89
|||||

RESULT 11

A2537061

LOCUS

DEFINITION

A2537061 456 bp DNA linear GSS 06-NOV-2000
AST-2P01514.AB Genetrap PC-3 Human Prostatic Carcinoma Library Homo

```

sapiens genomic 5', genomic survey sequence.
AZ537061      GI:11113828
VERSION      GSS.
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M.,
Bernardino,A., Durick,K. and Pollok,B.
Exon-trap tags from a PC-3 GenomeScreen(TM) Library
Unpublished (2000)
Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkelga@aurabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
preceded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAMP-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
Class: exon-trapped.
FEATURES
source      Location/Qualifiers
1..456
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Adenocarcinoma"
/cell_type="Epithelial"
/cell_line="PC-3"
/clone_lib="Genetrap PC-3 Human Prostatic Carcinoma
Library"
/notes="Organ: Prostate; Vector: pAMP-1; 3' RACE of total
RNA from genetrap pools; shotgun clone in pAMP-1 and used
to transform DH5-alpha competent bacteria."
ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTGGGGTGATGTGGAGC 18
|||||
Db      346 CCTGGGGTGATGTGGAGC 363

RESULT 12
CN422261/c
LOCUS      CN422261      474 bp mRNA linear EST 16-MAY-2004
DEFINITION      17000424524125 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
ACCESSION      CN422261
VERSION
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 474)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murgue,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)

FEATURES
source      Location/Qualifiers
1..475
/organism="Homo sapiens"
/mol_type="mRNA"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN EB"
/notes="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 7; Length 474;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTGGGGTGATGTGGAGC 18
|||||
Db      408 CCTGGGGTGATGTGGAGC 391

RESULT 13
BQ331598/c
LOCUS      BQ331598      475 bp mRNA linear EST 17-MAY-2002
DEFINITION      MR4-ET0138-080501-010-d06 ET0138 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BQ331598
VERSION      BQ331598.1 GI:20972765
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 475)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR4&t2=MR4-ET0138-
080501-010-d06&t3=2001-05-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 41
High quality sequence stop: 475.
FEATURES
source      Location/Qualifiers
1..475
/organism="Homo sapiens"
/mol_type="mRNA"

```

```

COMMENT      Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 474 Std Error: 0.00.
Location/Qualifiers
1..474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN EB"
/notes="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 7; Length 474;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTGGGGTGATGTGGAGC 18
|||||
Db      408 CCTGGGGTGATGTGGAGC 391

RESULT 13
BQ331598/c
LOCUS      BQ331598      475 bp mRNA linear EST 17-MAY-2002
DEFINITION      MR4-ET0138-080501-010-d06 ET0138 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BQ331598
VERSION      BQ331598.1 GI:20972765
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 475)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR4&t2=MR4-ET0138-
080501-010-d06&t3=2001-05-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 41
High quality sequence stop: 475.
FEATURES
source      Location/Qualifiers
1..475
/organism="Homo sapiens"
/mol_type="mRNA"

```

/db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ET0138"
 Note: Organ: lung tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No.196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 475;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18
 ||||||||||||||||
 Db 242 CCTGGGGTGATGTGGAGC 225

RESULT 14
 BM050133/c
 LOCUS 478 bp mRNA linear EST 07-NOV-2001
 DEFINITION 603632480F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5422338 5',
 mRNA sequence.

ACCESSION BM050133

VERSION BM050133.1 GI:16779400

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 478)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rc@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM1879 row: p column: 19

High quality sequence stop: 267.

Location/Qualifiers

1. 478

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5422338"

/tissue_type="epithelioid carcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC 42"

/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 478;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18

Db 90 CCTGGGGTGATGTGGAGC 73
 ||||||||||||||||

RESULT 15

AW814883

LOCUS 486 bp mRNA linear EST 17-MAY-2000

DEFINITION MR1-ST0206-120400-022-f04 ST0206 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW814883

VERSION AW814883.1 GI:7907877

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 486)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MR1-ST0206-120>

400-022-f04&t3=2000-04-12&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 55

High quality sequence stop: 485.

FEATURES

" source

1. 486

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="ST0206"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No.196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 486;

Best Local Similarity 100.0%; Pred. No. 6.1e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18

||||||||||||||||

Db 339 CCTGGGGTGATGTGGAGC 356

Search completed: February 5, 2005, 08:11:51

Job time : 2148.2 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-11
Perfect score: 18
Sequence: 1 agtccacaaaagtatccc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_ptg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235159
2	18	100.0	18	6	BD235178
3	18	100.0	18	6	BD235179
4	18	100.0	387	6	CQ732731
5	18	100.0	587	6	CQ09589
6	18	100.0	587	6	CQ138575
7	18	100.0	587	6	CQ175406
8	18	100.0	587	6	CQ221990
9	18	100.0	587	6	CQ25935
10	18	100.0	587	6	CQ297711
11	18	100.0	587	6	CQ334058
12	18	100.0	636	6	BD097037
13	18	100.0	702	6	BD084108
14	18	100.0	702	6	BD102202
15	18	100.0	702	9	BT007208
16	18	100.0	702	12	BT008248
17	18	100.0	737	6	AR054022
18	18	100.0	737	6	AR172595
19	18	100.0	737	6	I52012

c 20	18	100.0	737	6	AR371662
c 21	18	100.0	737	6	AR380913
c 22	18	100.0	737	9	HSBCLXS
c 23	18	100.0	747	6	AX127722
c 24	18	100.0	926	6	AR054021
c 25	18	100.0	926	6	AR118504
c 26	18	100.0	926	6	AR124952
c 27	18	100.0	926	6	AR144311
c 28	18	100.0	926	6	AR172594
c 29	18	100.0	926	6	BD243042
c 30	18	100.0	926	6	CQ765842
c 31	18	100.0	926	6	CQ58777
c 32	18	100.0	926	6	I52011
c 33	18	100.0	926	6	AR371661
c 34	18	100.0	926	6	AR380885
c 35	18	100.0	926	6	AX839772
c 36	18	100.0	926	6	AX925686
c 37	18	100.0	926	9	HSBCLXL
c 38	18	100.0	1163	4	AB080951
c 39	18	100.0	1236	6	AX085490
c 40	18	100.0	1252	4	AB073983
c 41	18	100.0	1455	6	AX085496
c 42	18	100.0	2575	6	CQ827863
c 43	18	100.0	2575	9	BC019307
c 44	18	100.0	7372	6	E23357
c 45	18	100.0	99593	9	HSJ857M17

ALIGNMENTS

BD235159 18 bp DNA linear PAT 17-JUL-2003
Oligonucleotide inhibitors of bcl-xL.

BD235159
BD235159.1 GI:33044929
JP 2002519048-A/11.

synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 18)
Stein,C.A.

Oligonucleotide inhibitors of bcl-xL
Patent: JP 2002519048-A 11 02-JUL-2002;

THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

OS Artificial Sequence

PN JP 2002519048-A/11

PD 02-JUL-2002

PF 02-JUL-1999 JP 2000557839

PI 02-JUL-1998 US 09/109614

PI CY A STEIN

PC

C12N15/09,A61K9/127,A61K31/711,A61K31/712,A61K31/7125, PC

A61K47/42,

PC A61K47/48,A61K48/00,A61P35/00,C12N15/00

CC ANTISENSE OLIGONUCLEOTIDE

Location/Qualifiers

FT key 1..18

/organism='Artificial Sequence'

FT Location/Qualifiers

1..18

/organism='synthetic construct'

/mol_type='genomic DNA'

/db_xref='taxon:32630'

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18

|||||

```

Db          1 AGTTCACAAAAGTATCC 18

RESULT 2
BD235178
LOCUS      18 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235178
VERSION     BD235178.1 GI:33044948
KEYWORDS   JP 2002519048-A/30.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 31 02-JUL-2002;
            THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
            PN JP 2002519048-A/31
            PD 02-JUL-2002
            PF 02-JUL-1999 JP 2000557839
            PR 02-JUL-1998 US 09/109614
            PI CY A STEIN
PC         C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
            A61K47/42,
            PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
            CC ANTISENSE OLIGONUCLEOTIDE
            CC PHOSPHOROTHIOATE LINKAGE
            CC PHOSPHOROTHIOATE LINKAGE
            CC PHOSPHOROTHIOATE LINKAGE
            CC PHOSPHOROTHIOATE LINKAGE
            FH key      Location/Qualifiers
            FT misc_binding (1)..(4)
            FT misc_binding (5)..(6)
            FT misc_binding (8)..(9)
            FT misc_binding (14)..(18).
FEATURES   source
            Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTTCACAAAAGTATCC 18
        |||||
DB       1 AGTTCACAAAAGTATCC 18
        |||||

RESULT 4
CQ732731/c
LOCUS      387 bp      DNA      linear      PAT 03-FEB-2004
DEFINITION Sequence 18665 from Patent WO02068579.
ACCESSION  CQ732731
VERSION     CQ732731.1 GI:42313858
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
TITLE      Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
JOURNAL    Patent: WO 02068579-A 18665 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES   source
            Location/Qualifiers
            1..387
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTTCACAAAAGTATCC 18
        |||||
DB       1 AGTTCACAAAAGTATCC 18
        |||||

RESULT 3
BD235179
LOCUS      18 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235179
VERSION     BD235179.1 GI:33044949
KEYWORDS   JP 2002519048-A/31.

```



```

QY 1 AGTTCACAAAAGTATCC 18
Db 266 AGTTCACAAAAGTATCC 249

RESULT 5
LOCUS CQ099589
DEFINITION Sequence 8448 from Patent WO0157272.
ACCESSION CQ099589
VERSION CQ099589.1 GI:41068615
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
JOURNAL analysis of gene expression in human placenta
Patent: WO 0157272-A 8448 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL = 1.5"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

RESULT 6
LOCUS CQ138575
DEFINITION Sequence 8597 from Patent WO0157276.
ACCESSION CQ138575
VERSION CQ138575.1 GI:41095941
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
JOURNAL analysis of gene expression in human bone marrow
Patent: WO 0157276-A 8597 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL = 5.5"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

RESULT 7
LOCUS CQ175406
DEFINITION Sequence 6802 from Patent WO0157274.
ACCESSION CQ175406
VERSION CQ175406.1 GI:41170145
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
JOURNAL analysis of gene expression in human heart
Patent: WO 0157274-A 6802 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.6"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

RESULT 8
LOCUS CQ221990
DEFINITION Sequence 8829 from Patent WO0157273.
ACCESSION CQ221990
VERSION CQ221990.1 GI:41204114
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 27 September 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 8829 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL = 1.9"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

```

```
QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

RESULT 9
LOCUS CQ259935 587 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 8196 from Patent WO0157277.
ACCESSION CQ259935
VERSION CQ259935.1 GI:41232415
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
JOURNAL Human genome-derived single exon nucleic acid probes useful for
FEATURES analysis of gene expression in human fetal liver
source Patent: WO 0157277-A 8196 09-AUG-2001;
Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
= 4.1"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

RESULT 10
LOCUS CQ297711 587 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 8816 from Patent WO0186003.
ACCESSION CQ297711
VERSION CQ297711.1 GI:41258288
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
JOURNAL Human genome-derived single exon nucleic acid probes useful for
FEATURES analysis of gene expression in human lung
source Patent: WO 0186003-A 8816 15-NOV-2001;
Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL = 2.2"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527
```

```
RESULT 11
LOCUS CQ334058 587 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 8152 from Patent WO0157275.
ACCESSION CQ334058
VERSION CQ334058.1 GI:41283090
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
JOURNAL Human genome-derived single exon nucleic acid probes useful for
FEATURES analysis of gene expression in human brain
source Patent: WO 0157275-A 8152 09-AUG-2001;
Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL = 2"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

RESULT 12
LOCUS BD097037/c 636 bp DNA linear PAT 27-AUG-2002
DEFINITION A BH4 fusion polypeptide.
ACCESSION BD097037
VERSION BD097037.1 GI:22642625
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 636)
AUTHORS Shimizu, S. and Tsujimoto, Y.
TITLE A BH4 fusion polypeptide
JOURNAL Patent: WO 0148014-A 3 05-JUL-2001;
COMMENT SHIONOGI & CO LTD, SHIGEMI SHIMIZU, YOSHIHI TSUJIMOTO
OS Artificial Sequence
PN WO 0148014-A/3
PD 05-JUL-2001
PF 26-DEC-2000 WO 2000JP009274
PI 27-DEC-1999 JP 99P 371449
PR SHIGEMI SHIMIZU, YOSHIHI TSUJIMOTO
PC C07K14/47, C12N15/12, A61K38/17, A61P9/10
CC Synthesized DNA for mutant bcl-x L.
FH Key Location/Qualifiers
FT CDS (1)..(636).
Location/Qualifiers
1..636
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527
```

Db 518 AGTCCACAAAAGTATCC 501

RESULT 13
BD084108/c
LOCUS BD084108 702 bp DNA linear PAT 27-AUG-2002
DEFINITION Method of detecting protein-protein interaction.
ACCESSION BD084108
VERSION BD084108.1 GI:22629718
KEYWORDS JP 2001327296-A/7.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kato, S., Eguchi, C. and Nagata, N.
TITLE Method of detecting protein-protein interaction
AUTHORS Kato, S., Eguchi, C. and Nagata, N.
JOURNAL Patent: JP 2001327296-A 7 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001327296-A/7
PD 27-NOV-2001
PF 24-AUG-2000 JP 2000254418
PI SEISHI KATO, CHIKASHI EGUCHI, NAOKI NAGATA
PC C12N15/09, C12Q1/02, C07K14/47, (C12N15/09, C12R1:91), (C12Q1/02,
C12R1:91),
PC C12N15/00, (C12N15/00, C12R1:91)
CC Method of detecting protein-protein interaction FH Key
CDS Location/Qualifiers
FT CDS (1)..(702).

FEATURES
source
1..702
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTCCACAAAAGTATCC 18
|||||
Db 581 AGTCCACAAAAGTATCC 564
|||||

RESULT 15
BD007208/c
LOCUS BD007208 702 bp mRNA linear PRI 13-MAY-2003
DEFINITION Homo sapiens BCL2-like 1 mRNA, complete cds.
ACCESSION BD007208
VERSION BD007208.1 GI:30583254
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kainine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labaer, J., Lin, Y.,
Phelan, M. and Farmer, A.
TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 702)
AUTHORS Kainine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labaer, J., Lin, Y.,
Phelan, M. and Farmer, A.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA
COMMENT This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the Sali and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sali site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.

FEATURES
source
1..702
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GH00804X1.0"
/clone_lib="BD Creator(TM) CDS Library derived from MGC
collection"
/lab_host="DH5alpha T1 resistant"
/notes="Vector: pDNR-Dual"
1..702
/codon_start=1
/product="BCL2-like 1"
/protein_id="AAP35872.1"
/db_xref="GI:30583255"

CDS
1..702
/product="BCL2-like 1"
/protein_id="AAP35872.1"
/db_xref="GI:30583255"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTCCACAAAAGTATCC 18
|||||
Db 581 AGTCCACAAAAGTATCC 564
|||||

RESULT 14
BD102202/c
LOCUS BD102202 702 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting protein-protein interaction.
ACCESSION BD102202
VERSION BD102202.1 GI:22647776
KEYWORDS WO 0168885-A/7.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kato, S., Eguchi, C., Nagata, N. and Otake, M.
TITLE Method for detecting protein-protein interaction
AUTHORS Kato, S., Eguchi, C., Nagata, N. and Otake, M.
JOURNAL Patent: WO 0168885-A 7 20-SEP-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP, SEISHI KATO, CHIKASHI EGUCHI, NAOKI
NAGATA, MIYAKO OTAKE
COMMENT OS Homo sapiens (human)
PN WO 0168885-A/7
PD 20-SEP-2001
PF 15-MAR-2000 WO 2001JP001973
PI SEISHI KATO, CHIKASHI EGUCHI, NAOKI NAGATA, MIYAKO OTAKE PC
C12N15/79, G01N33/68, C12P21/02, C07K19/00
CC Method for detecting protein-protein interaction FH Key
CDS Location/Qualifiers
FT CDS (1)..(702).

Query Match 100.0%; Score 18; DB 9; Length 702;
Best Local Similarity 100.0%; Fred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCCACAAAAGTATCC 18
|||||
Db 581 AGTTCCACAAAAGTATCC 564

Search completed: February 4, 2005, 23:30:42
Job time : 433.664 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169A-11
Perfect score: 18
Sequence: 1-agtccacaaagtatcc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	Az46981 Bcl-XL mr
2	18	100.0	179	12	Ach84269 Human gen
3	18	100.0	337	10	Adk66037 Standardi
4	18	100.0	492	9	Ach46093 Human inf
5	18	100.0	587	4	Aba59891 Human foe
6	18	100.0	587	4	Aai39762 Probe #84
7	18	100.0	587	4	Aba28336 Probe #68
8	18	100.0	587	4	Aak34040 Human bon
9	18	100.0	587	4	Aak08161 Human bra
10	18	100.0	587	4	Abs33839 Human liv
11	18	100.0	587	6	Abs08825 Human gen
12	18	100.0	587	12	Ach70569 Human gen
13	18	100.0	636	4	Aah48169 Mutant bc
14	18	100.0	702	5	Aah43464 cDNA clon
15	18	100.0	702	12	Adm45994 Human apo
16	18	100.0	737	2	Aaq81699 Human thy
17	18	100.0	737	10	Abz83507 Toxilog
18	18	100.0	737	11	Adi32132 Human cdn
19	18	100.0	739	12	Adg52218 Human bcl
20	18	100.0	747	4	Aaf30926 Human bcl
21	18	100.0	747	12	Adg65209 Human Bcl

c	22	18	100.0	926	2	AAQ81698	Aaq81698 Human thy
c	23	18	100.0	926	2	AAT40079	Aat40079 Bcl-XL ge
c	24	18	100.0	926	3	AAZ93614	Aaz93614 Bcl-x gen
c	25	18	100.0	926	4	AAS15189	Aas15189 Human bcl
c	26	18	100.0	926	4	AAC90810	Aac90810 Human bcl
c	27	18	100.0	926	6	ABK84766	Abk84766 Human cdn
c	28	18	100.0	926	8	ABT16641	Abt16641 Human bcl
c	29	18	100.0	926	10	ADD56779	Add56779 Human bcl
c	30	18	100.0	926	10	AAD64187	Aad64187 Human bcl
c	31	18	100.0	926	11	ADI32104	Adi32104 Human cdn
c	32	18	100.0	926	12	ADH52630	Adh52630 Human ant
c	33	18	100.0	926	12	ADO19990	Ado19990 Human pro
c	34	18	100.0	926	12	ADP13351	Adp13351 Renal cel
c	35	18	100.0	1236	5	AAS00247	Aas00247 Bcl-XL-DT
c	36	18	100.0	1455	5	AAS00250	Aas00250 LFN-Bcl-X
c	37	18	100.0	2386	10	ADG89403	Adg89403 Cancer de
c	38	18	100.0	2386	12	ADN04260	Adn04260 Antipsori
c	39	18	100.0	2575	12	ADO19866	Ado19866 Human PRO
c	40	18	100.0	7372	2	AAX33182	Aax33182 Base sequ
	41	17.2	95.6	20	3	AAC65053	Aac65053 Human bcl
	42	17	94.4	20	3	AAZ93647	Aaz93647 Antisense
	43	17	94.4	20	4	AAS15196	Aas15196 Human bcl
	44	17	94.4	20	5	AAH27692	Aah27692 Human bcl
	45	17	94.4	20	6	ABV73654	Abv73654 Human bcl

ALIGNMENTS

RESULT 1
AAZ46981
ID AAZ46981 standard; DNA; 18 BP.
XX AC AAZ46981;
XX AC AAZ46981;
DT 14-APR-2000 (first entry)
XX DE Bcl-XL mRNA specific antisense oligo K.
XX DE Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.
XX KW Homo sapiens.
XX OS WO200001393-A2.
XX PN 13-JAN-2000.
XX PF 02-JUL-1999; 99WO-US015250.
XX PR 02-JUL-1998; 98US-00109614.
XX PR (UYCO) UNIV COLUMBIA NEW YORK.
XX PI Stein CA;
XX WPI; 2000-137140/12.
XX PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-
PT XL, useful for reducing bcl-xL production in tumor cells to treat cancer
or in vascular cells to promote the regression of vascular lesions.
XX PS Claim 1; Fig 1; 69pp; English.
XX CC The invention provides antisense oligonucleotides or their derivatives
CC which reduce or eliminate expression of the anti-apoptotic protein bcl-
CC XL. The oligonucleotides can be introduced into tumour cells to reduce
CC bcl-xL production to treat cancer, especially epithelial cancer, e.g.
CC prostate, lung or bladder cancer. Oligonucleotides comprising one or more
CC bases with a C-5 propynyl pyrimidine modification may especially be used
CC to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in
CC such treatment. The oligonucleotides can be introduced into vascular
CC cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
 CC represent antisense oligos specific for the bcl-X1 mRNA

XX Sequence 18 BP; 7 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAAGTATCC 18
 Db 1 AGTTCACACAAAAGTATCC 18

RESULT 2

ACH84269/c
 ID ACH84269 standard; DNA; 179 BP.

XX ACH84269;
 AC ACH84269;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #17464.

XX Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

PD 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

XX Claim 1; SEQ ID NO 17464; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 179 BP; 37 A; 53 C; 48 G; 41 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 179;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAAGTATCC 18

Db 37 AGTTCACACAAAAGTATCC 20

RESULT 3

ADK66037/c

ID ADK66037 standard; DNA; 337 BP.

XX ADK66037;

DT 06-MAY-2004 (first entry)

XX Standardized polynucleotide system polynucleotide #8.

XX ss; standardized polynucleotide system; medical diagnosis;
 KW functional genomics; sample analysis; pharmacogenomics; sample analysis.
 XX Unidentified.

XX DE10209071-A1.

XX 25-SEP-2003.

XX 28-FEB-2002; 2002DE-01009071.

XX 28-FEB-2002; 2002DE-01009071.

XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.

XX Koehler T, Rost A;

XX WPI; 2003-732912/70.

XX Standardized polynucleotide system, useful for quantitative, real-time
 PT determination of nucleic acid, comprises stabilized standards, primers
 PT and probe.

XX Claim 1; Page 7; 38pp; German.

XX The present invention relates to a standardized polynucleotide system,
 CC which comprises at least one carrier nucleic acid, at least 3
 CC oligonucleotides, as primers and target-specific, fluorescently labeled
 CC probe and optionally at least one set of stabilized controls (standard
 CC RNA or DNA) of known concentration and instructions. The system comprises
 CC any of 20 sets of one control, two primers and one target-specific probe.
 CC The standardized polynucleotide system can be used for quantitative, real
 CC -time detection of target nucleic acids, especially analysis of genes or
 CC gene products, e.g. for individualized medical diagnosis, in veterinary
 CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,

CC Pharmaceutical testing, analysis of food or environmental samples and
CC also for ultra-sensitive detection of proteins by immuno-PCR. The present
CC sequence is a polynucleotide used in the system of the invention.
SQ Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 337;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCCACAAAAGTATCC 18
|||
Db 178 AGTTCCACAAAAGTATCC 161

RESULT 4
ACH46093/C
ID ACH46093 standard; cDNA; 492 BP.

AC ACH46093;

XX 13-OCT-2003 (first entry)

XX Human infant brain cDNA #156.

XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.

XX Homo sapiens.

XX US2003073623-A1.

XX 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.

XX 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.

XX (LABA/) LABAT I.

XX (STAC/) STACHE-CRAIN B.

XX (DICK/) DICKSON M C.

XX (JONE/) JONES L W.

XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.

PS Claim 1; SEQ ID NO 33305; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present polypeptide
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030073623

SQ Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 9; Length 492;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCCACAAAAGTATCC 18
|||
Db 362 AGTTCCACAAAAGTATCC 345

RESULT 5
ABA59891
ID ABA59891 standard; DNA; 587 BP.

XX ABA59891;

XX 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #8196.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GE-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human foetal liver.

PS Claim 1; SEQ ID NO 8196; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human foetal liver. The
XX present sequence is a single exon nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCCACAAAAGTATCC 18
|||
Db 510 AGTTCCACAAAAGTATCC 527

RESULT 6
AAI39762
ID AAI39762 standard; DNA; 587 BP.

```

XX AC AAI39762;
XX DT 17-OCT-2001 (first entry)
XX DE Probe #8448 used to measure gene expression in human placenta sample.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488897/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human placenta.
XX PS Claim 25; SEQ ID NO 8448; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP).
XX CC The present sequence is one such probe. The probes are useful for
XX CC producing a microarray for predicting, measuring and displaying gene
XX CC expression in samples derived from human placenta. The probes are useful
XX CC for antenatal diagnosis of human genetic disorders
XX SQ Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAGTATCC 18
DB 510 AGTTCACACAAAGTATCC 527

RESULT 7
ABR28336
ID ABA28336 standard; DNA; 587 BP.
XX AC ABA28336;
XX DT 23-JAN-2002 (first entry)
XX DE Probe #6802 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.

```

```

XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488899/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 1; SEQ ID NO 6802; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease. Note: The sequence data for this patent did not
XX CC form part of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAGTATCC 18
DB 510 AGTTCACACAAAGTATCC 527

RESULT 8
AAK34040
ID AAK34040 standard; DNA; 587 BP.
XX AC AAK34040;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 8597.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.

```


CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention

XX Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 18; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 AGTTCACAAAAAGCTATCC 18
| | | | | | | | | | | |
Db 510 AGTTCACAAAAAGTATCC 527

RESULT 10
ABS33839
ID ABS33839 standard; DNA; 587 BP.
XX AC
XX ABS33839;
XX AC
XX DT
XX 25-FEB-2003 (first entry)
XX DE Human liver single exon probe, SEQ ID NO 8829.
XX DE
XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX KW
XX OS Homo sapiens.
XX OS
XX WO200157273-A2.
XX PN
XX 09-AUG-2001.
XX PD
XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX PR
XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX PS
XX Claim 1; SEQ ID NO 8829; 658pp; English.

CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABSS1005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 587;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAAGTATCC 18
 DB 510 AGTTCACACAAAAGTATCC 527

RESULT 11
 ABS08825
 ID ABS08825 standard; DNA; 587 BP.
 AC ABS08825;
 DT 19-AUG-2002 (first entry)
 XX Human genome-derived single exon probe from lung SEQ ID NO 8816.
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200186003-A2.
 XX 15-NOV-2001.
 XX 30-JAN-2001; 2001WO-US000665.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234887P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX Claim 1; SEQ ID NO 8816; 634pp; English.

The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridize at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a single exon probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 18; DB 6; Length 587;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAAGTATCC 18
 DB 510 AGTTCACACAAAAGTATCC 527

RESULT 12
 ACH70569/c
 ID ACH70569 standard; DNA; 587 BP.
 XX ACH70569;
 XX 29-JUL-2004 (first entry)
 DT 29-JUL-2004 (first entry)
 XX Human genome derived single exon probe #3764.
 DE Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 KW Homo sapiens.
 OS Homo sapiens.
 XX US2003194704-A1.
 XX 16-OCT-2003.
 PD 03-APR-2002; 2002US-00029386.
 PF 03-APR-2002; 2002US-00029386.
 PR 03-APR-2002; 2002US-00029386.
 XX (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX Penn SG, Rank DR, Hanzel DK;
 PI WPI; 2004-119264/12.
 XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX Claim 15; SEQ ID NO 3764; 80pp; English.

CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subsequence, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above). The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030194704

XX SQ Sequence 587 BP; 130 A; 193 C; 129 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 587;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCCACAAAGTATCC 18
 |||||
 Db 78 AGTTCCACAAAGTATCC 61

RESULT 13
 AAH48169/c
 ID AAH48169 standard; DNA; 636 BP.

XX AC AAH48169;

XX DT 21-SEP-2001 (first entry)

XX DE Mutant bcl-XL coding sequence.

XX KW BH4 domain; cardiant; anti-HIV; neuroprotective; hepatotropic; Bcl-2;
 KW antidiabetic; apoptosis inhibitor; cellular uptake; anti-apoptosis;
 KW ischaemic disease; myocardial infarct; AIDS; neurodegenerative diseases;
 KW infective multiple failure; fulminant hepatitis; diabetes; mutant;
 KW Bcl-XL; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200148014-A1.

XX PD 05-JUL-2001.

XX FF 26-DEC-2000; 2000WO-JP009274.

XX PR 27-DEC-1999; 99JP-00371449.

XX PA (SHIO) SHIONOGI & CO LTD.

XX PI Shimizu S, Tsujimoto Y;

XX DR WPI; 2001-418246/44.

XX DR P-PSDB; AAG64285.

XX BH4-fused polypeptides with peptide sequences capable of exerting effect
 PT on enabling uptake into cells, applicable as effective apoptosis
 PT inhibitors, useful in preventives or remedies for ischemic diseases e.g.
 PT myocardial infarct.

XX PS Disclosure; Page 66-68; 84pp; Japanese.

XX The present invention relates to BH4-fused polypeptides. The BH4-fused
 CC polypeptide have a sequence capable of affecting cellular uptake and also
 CC a BH4 domain sequence from an anti-apoptosis Bcl-2 family protein. The
 CC BH4-fused polypeptides are useful as effective apoptosis inhibitors, and
 CC are useful in preventives or remedies for ischaemic diseases e.g.
 CC myocardial infarct, AIDS, neurodegenerative diseases, infective multiple
 CC failure, fulminant hepatitis and diabetes. The present sequence is a
 CC mutant bcl-XL sequence which was used in the present invention. This
 CC sequence was derived from a human bcl-XL DNA sequence

XX SQ Sequence 636 BP; 148 A; 158 C; 207 G; 123 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 636;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCCACAAAGTATCC 18
 |||||
 Db 518 AGTTCCACAAAGTATCC 501

RESULT 14

AAH43464/c

ID AAH43464 standard; cDNA; 702 BP.

XX AC AAH43464;

XX DT 04-DEC-2001 (first entry)

XX DE cDNA clone HP03564 ORF.

XX KW Npw38; NpwBP; protein interaction; reporter function; eukaryotic cell;
 KW localization; protein network; intracellular; primer; amplify; PCR;
 KW polymerase chain reaction; mitochondria; ss.

XX OS Homo sapiens.

XX FN WO200168885-A1.

XX PD 20-SEP-2001.

XX PF 13-MAR-2001; 2001WO-JP001973.

XX PR 15-MAR-2000; 2000JP-00073095.

XX PR 24-AUG-2000; 2000JP-00254418.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Kato S, Eguchi C, Nagata N, Otake M;

XX DR WPI; 2001-590069/66.

XX DR P-PSDB; AAB47515.

XX PT Detection of protein-protein interactions for screening compounds capable
 PT of modifying the interaction comprises observing intracellular
 PT localization of one protein after altering the modification pattern.

XX PS Example 6; Page 27-29; 33pp; Japanese.

XX This sequence represents the open reading frame of the mitochondrial cDNA
 CC clone HF03564. The protein encoded by this sequence was used in the
 CC method of the invention. The method allows detection of interactions
 CC between a protein X and a protein Y which has a reporter function in
 CC eukaryotic cells, and comprises modifying the localization patterns of X
 CC and/or Y, and the localization of Y in the cell is observed using the
 CC reporter function. This method is useful for the elucidation of protein
 CC networks within the cell. It is also applicable for the discovery of new
 CC proteins and low-molecular drugs, by observing their effect on
 CC intracellular protein interactions
 XX
 SQ Sequence 702 BP; 165 A; 175 C; 224 G; 138 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 5; Length 702;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAAGTATCC 18
 Db 581 AGTTCACACAAAAGTATCC 564

RESULT 15
 ADM45994/c
 ID ADM45994 standard; cDNA; 702 BP.

XX
 AC ADM45994;

XX
 DT 03-JUN-2004 (first entry)

XX Human apoptosis inhibitory factor Bcl-xL cDNA.

XX random oligonucleotide library; protein interaction; ligand;
 KW receptor binding site; ss; gene; human; apoptosis inhibitory factor;
 KW Bcl-xL.

XX Homo sapiens.

XX Key Location/Qualifiers

FF CDS 1..702

FT /*tag= a

FT /product= "Human apoptosis inhibitory factor Bcl-xL
 protein"

XX JP2004024078-A.

XX 29-JAN-2004.

XX 24-JUN-2002; 2002JP-00183456.

XX 24-JUN-2002; 2002JP-00183456.

XX (SERE-) SERESUTA REKISHIKO SCI KK.

XX WPI; 2004-161478/16.

DR P-PSDB; ADM45995.

XX Random oligonucleotide useful for detecting protein interaction, having
 PT base sequence, where each base of 1st and 2nd of the codon is the any of
 PT G, C, T (U), or A and the base of 3rd of codon is G or C, or G or T (U).

PS Example 2; SEQ ID NO 3; 43pp; Japanese.

XX The invention relates to a novel random oligonucleotide having a base
 CC sequence where each base of the 1st and 2nd codon is any of G, C, T (U)
 CC or A and each base of the 3rd codon is G or C, or G or T (U). The methods
 CC of the invention may be useful for preparing a random oligonucleotide
 CC preparation to be used for detecting protein interactions or for
 CC screening ligand or receptor protein binding sites. The current sequence
 CC is that of the human apoptosis inhibitory factor Bcl-xL cDNA of the
 CC invention.

SQ Sequence 702 BP; 165 A; 175 C; 224 G; 138 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 12; Length 702;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAAGTATCC 18
 Db 581 AGTTCACACAAAAGTATCC 564

Search completed: February 4, 2005, 21:52:43
 Job time : 232.23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-11
Perfect score: 18
Sequence: 1 agttccacaaaagtatcc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	167	2	BF929309 IL2-NT020
2	18	100.0	216	2	BF806802 PM2-C1011
3	18	100.0	231	4	BM818607 K-EST0085
4	18	100.0	232	2	BF804861 PM2-C1011
5	18	100.0	256	4	BM049697 603624202
6	18	100.0	283	2	BF823588 RCS-RT005
7	18	100.0	332	2	AW820481 QV2-ST029
8	18	100.0	358	2	AW820530 QV2-ST029
9	18	100.0	396	4	BM818649 K-EST0085
10	18	100.0	418	4	BI051278 CM3-GN029
11	18	100.0	418	4	BM741875 K-EST0014
12	18	100.0	442	1	AA903741 ok64a12.8
13	18	100.0	447	4	BM818387 K-EST0085
14	18	100.0	482	2	BE378810 601237325
15	18	100.0	486	2	AW814883 MRI-ST020
16	18	100.0	516	7	HO9884 Ym05007.r1
17	18	100.0	522	2	BE395937 601312716
18	18	100.0	555	2	BE393580 601310279
19	18	100.0	563	2	BE617040 601441454
20	18	100.0	579	4	BM741157 K-EST0013
21	18	100.0	607	5	BQ636684 hdl3a09.y
22	18	100.0	620	4	BM820164 K-EST0088
23	18	100.0	652	4	BM043798 603620649
24	18	100.0	657	2	BE207063 ba09f05.y

c	25	18	100.0	681	6	CF147016 UI-HF-CB0
c	26	18	100.0	687	2	BE293685 601186941
c	27	18	100.0	695	4	BI252492 602952957
c	28	18	100.0	697	4	BI457116 603185360
c	29	18	100.0	699	2	BE870269 601447403
c	30	18	100.0	705	4	EG290422 602389270
c	31	18	100.0	714	4	EG470667 602511594
c	32	18	100.0	720	6	CD636470 56049223J
c	33	18	100.0	725	6	CD636468 56049107J
c	34	18	100.0	737	4	BG748447 602706419
c	35	18	100.0	765	2	BF569393 602185659
c	36	18	100.0	767	2	BE512918 601172142
c	37	18	100.0	782	2	BE249973 600943141
c	38	18	100.0	798	5	BQ687097 AGENCOURT
c	39	18	100.0	798	5	BUS28551 AGENCOURT
c	40	18	100.0	798	7	CK000319 AGENCOURT
c	41	18	100.0	808	4	BI222971 602943462
c	42	18	100.0	817	5	BQ943707 AGENCOURT
c	43	18	100.0	830	7	CF619432 AGENCOURT
c	44	18	100.0	843	5	BQ921211 AGENCOURT
c	45	18	100.0	843	5	BQ962018 AGENCOURT

ALIGNMENTS

RESULT 1
BF929309
LOCUS 167 bp mRNA linear EST 19-JAN-2001
DEFINITION IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF929309
VERSION BF929309.1 GI:12327437
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 167)
AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Dias Neto,E., Garcia Correea,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc.Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 167.
Location/Qualifiers
1. .167
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0202"
/notes="Organ: nervous tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 AGTTCACAAAAGTATCC 18
|||||
DB 147 AGTTCACAAAAGTATCC 164

RESULT 2

BF806802 216 bp mRNA linear EST 12-JAN-2001
LOCUS PM2-CI0111-091100-004-b10 CI0111 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF806802
ACCESSION BF806802
VERSION BF806802.1 GI:12135791
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, U.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PubMed 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-091100-004-b10&t3=2000-11-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 216.

FEATURES

source

1..216
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CI0111"
/notes="Organ: colon ins; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
Derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
|||||
DB 146 AGTTCACAAAAGTATCC 163

RESULT 3

BF818607 231 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0085942 S20T665307 Homo sapiens cDNA clone S20T665307-4-B02
DEFINITION 5', mRNA sequence.

ACCESSION BF818607
VERSION BF818607.1 GI:19175020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 231)

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 Row: B Column: 02
High quality sequence stop: 231.

FEATURES

source

1..231
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-4-B02"
/sex="M"
/lab_host="Top10F"
/clone_lib="S20T665307"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
|||||
DB 215 AGTTCACAAAAGTATCC 198

RESULT 4

BF804861 232 bp mRNA linear EST 12-JAN-2001
LOCUS PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF804861
ACCESSION BF804861

VERSION BF804861.1 GI:12133850
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 232)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&tl2=PM2-CI0111-041100-001-401&tl3=2000-11-04&tl4=1)

Seq primer: puc 18 forward
 High quality sequence start: 13
 High quality sequence stop: 232.

FEATURES source
 Location/Qualifiers
 1..232
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="CI0111"
 /note="Organ: colon ins; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Query Match 100.0%; Score 18; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAGTATCC 18
 |||||
 Db 162 AGTTCACAAAGTATCC 179

RESULT 5
 BM049697/c
 LOCUS 603624202F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5450041 5', mRNA sequence.
 DEFINITION
 ACCESSION BM049697
 VERSION BM049697.1 GI:16778964
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 256)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1938 row: c column: 02
 High quality sequence stop: 171.

FEATURES source
 Location/Qualifiers
 1..256
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5450041"
 /tissue_type="carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_40"
 /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 18; DB 4; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAGTATCC 18
 |||||
 Db 64 AGTTCACAAAGTATCC 47

RESULT 6
 BF823588
 LOCUS RC5-RT0055-221200-011-G02 RT0055 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BF823588
 VERSION BF823588.1 GI:12164528
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 283)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-221200-011-G02&t3=2000-12-22&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 283.

FEATURES

source
 1. .283
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="RT0055"

/note="Organ: Kidney tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGTTCACAAAAGTATCC 18
 |||||
 Db 192 AGTTCACAAAAGTATCC 209

RESULT 7

AW820481/c
 LOCUS 332 bp mRNA linear EST 17-MAY-2000
 DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW820481
 VERSION AW820481.1 GI:7913475
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 332)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-ST0298-140200-042-f12&t3=2000-02-14&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 332.

FEATURES

source
 1. .332
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ST0298"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGTTCACAAAAGTATCC 18
 |||||
 Db 182 AGTTCACAAAAGTATCC 165

RESULT 8

AW820530/c
 LOCUS 358 bp mRNA linear EST 17-MAY-2000
 DEFINITION QV2-ST0298-220200-061-d10 ST0298 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW820530
 VERSION AW820530.1 GI:7913524
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 358)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-ST0298-220200-061-d10&t3=2000-02-22&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 44

High quality sequence stop: 358.

FEATURES

source
 1. .358
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ST0298"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 358;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
|||||
Db 196 AGTTCACAAAAGTATCC 179

RESULT 9

BM818649/c

LOCUS BM818649 396 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0085991 S20T665307 Homo sapiens cDNA clone S20T665307-4-F03
5', mRNA sequence.

ACCESSION BM818649

VERSION BM818649.1 GI:19175062

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL

COMMENT Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 4 row: F column: 03

High quality sequence stop: 396.

FEATURES

source

1..396

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S20T665307-4-F03"

/sex="M"

/lab_host="Top10F"

/clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transfection of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 396;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18

|||||

Db 215 AGTTCACAAAAGTATCC 198

RESULT 10

BI051278

LOCUS

DEFINITION CM3-GN0297-110101-607-f03 GN0297 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI051278

VERSION BI051278.1 GI:14458808

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

1 (bases 1 to 418)

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-
110101-607-f03&t3=2001-01-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 418.
Location/Qualifiers
1..418
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0297"
/note="Organ: placenta normal; Vector: puc18; Site 1:
SmaI; Site 2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

FEATURES

source

1..418

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="GN0297"

/note="Organ: placenta normal; Vector: puc18; Site 1:
SmaI; Site 2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 418;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18

|||||

Db 144 AGTTCACAAAAGTATCC 161

RESULT 11

BM741875/c

LOCUS BM741875 418 bp mRNA linear EST 01-MAR-2002

DEFINITION K-EST0014589 S6SNU620 Homo sapiens cDNA clone S6SNU620-4-Col 5',
mRNA sequence.

ACCESSION BM741875

VERSION BM741875.1 GI:19063204

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS 1 (bases 1 to 418)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 Row: C Column: 01
High quality sequence stop: 418.
Location/Qualifiers
FEATURES
source
1..418
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S6SNU620-4-C01"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10P"
/clone_lib="S6SNU620"
/notes="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTTCACAAAAGTATCC 18
|||||
Db 87 AGTTCACAAAAGTATCC 70
RESULT 12
AA903741 442 bp mRNA linear EST 09-JUN-1998
LOCUS Ok64a12.s1 NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518718 3,
DEFINITION similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X. i, mRNA
sequence.
ACCESSION AA903741.1 GI:3038864
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 42)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 536 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
FEATURES
source
1..442
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1518718"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP_GC4"
/notes="Vector: pYT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia) digested with Not I and cloned
into the Not I and Eco RI sites of the modified pYT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 442;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTTCACAAAAGTATCC 18
|||||
Db 388 AGTTCACAAAAGTATCC 405
RESULT 13
BM818387 447 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0085558 S20T665307 Homo sapiens cDNA clone S20T665307-3-B02
DEFINITION 5', mRNA sequence.
ACCESSION BM818387
VERSION BM818387.1 GI:19174800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 3 Row: B Column: 02
High quality sequence stop: 447.
Location/Qualifiers
FEATURES
source
1..447
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-3-B02"
/sex="M"

```

/lab_host="Top10F"
 /clone_lib="S20T665307"
 /note="Organ: Stomach; Vector: pcns; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 447;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACAAAGATATCC 18
 |||||
 Db 215 AGTTCACAAAGATATCC 198

RESULT 14

BE378810/c
 LOCUS BE378810 482 bp mRNA linear EST 21-JUL-2000
 DEFINITION 601237325F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609126 5',
 mRNA sequence.

ACCESSION BE378810

VERSION BE378810.1 GI:9324175

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 482)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1CM263 row: b column: 07

High quality sequence start: 4

High quality sequence stop: 479.

FEATURES

source

1..482
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3609126"
 /tissue_type="endometrium, adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 44"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 482;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACAAAGATATCC 18
 |||||
 Db 153 AGTTCACAAAGATATCC 136

RESULT 15

AW814883
 LOCUS AW814883 486 bp mRNA linear EST 17-MAY-2000
 DEFINITION MRI-ST0206-120400-022-f04 ST0206 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW814883

VERSION AW814883.1 GI:7907877

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 486)
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MRI-ST0206-120

400-022-f04&t3=2000-04-12&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 55

High quality sequence stop: 485.

FEATURES

source

1..486
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ST0206"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 486;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACAAAGATATCC 18
 |||||
 Db 106 AGTTCACAAAGATATCC 123

Search completed: February 5, 2005, 08:11:52
Job time : 2147.2 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-12
Perfect score: 18
Sequence: 1 ctttcggctctcgctgc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235160
2	18	100.0	18	6	BD235180
3	18	100.0	18	6	BD235181
4	18	100.0	127	6	CQ112670
5	18	100.0	127	6	CQ151543
6	18	100.0	127	6	CQ185285
7	18	100.0	127	6	CQ234920
8	18	100.0	127	6	CQ272476
9	18	100.0	127	6	CQ310145
10	18	100.0	127	6	CQ346752
11	18	100.0	387	6	CQ732731
12	18	100.0	587	6	CQ099589
13	18	100.0	587	6	CQ138575
14	18	100.0	587	6	CQ175406
15	18	100.0	587	6	CQ221990
16	18	100.0	587	6	CQ259335
17	18	100.0	587	6	CQ297711
18	18	100.0	587	6	CQ334058
19	18	100.0	636	6	BD097037

c 20	18	100.0	702	6	BD084108
c 21	18	100.0	702	6	BD102202
c 22	18	100.0	702	9	BT007208
c 23	18	100.0	702	12	BT008248
c 24	18	100.0	737	6	AR054022
c 25	18	100.0	737	6	AR172595
c 26	18	100.0	737	6	IS2012
c 27	18	100.0	737	6	AR371662
c 28	18	100.0	737	6	AR380913
c 29	18	100.0	737	9	HSBCLXS
c 30	18	100.0	747	6	AX127722
c 31	18	100.0	926	6	AR054021
c 32	18	100.0	926	6	AR118504
c 33	18	100.0	926	6	AR124952
c 34	18	100.0	926	6	AR144311
c 35	18	100.0	926	6	AR172594
c 36	18	100.0	926	6	BD243042
c 37	18	100.0	926	6	CQ765842
c 38	18	100.0	926	6	E58777
c 39	18	100.0	926	6	IS2011
c 40	18	100.0	926	6	AR371661
c 41	18	100.0	926	6	AR380885
c 42	18	100.0	926	6	AX839772
c 43	18	100.0	926	6	AX925686
c 44	18	100.0	926	9	HSBCLXL
c 45	18	100.0	1236	6	AX085490

ALIGNMENTS

RESULT 1
LOCUS BD235160 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION BD235160
VERSION BD235160.1 GI:33044930
KEYWORDS JP 2002519048-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Stein,C.A.
TITLE Oligonucleotide inhibitors of bcl-xL
JOURNAL Patent: JP 2002519048-A 12 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT OS Artificial Sequence
PN JP 2002519048-A/12
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN
PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC A61K47/42,
A61K47/48,A61K48/00,A61P35/00,C12N15/00
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence',
Location/Qualifiers
1..18
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630',

FEATURES

source
1..18
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630',

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CTTTCGGCTCTCGCTGC 18
|||||

1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 5

CQ151543
LOCUS
DEFINITION Sequence 21565 from Patent WO0157276.
ACCESSION CQ151543
VERSION CQ151543.1 GI:41158893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 21565 09-AUG-2001;
Acemica, Inc. (US)

FEATURES
source

1..127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 5.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 6

CQ185285
LOCUS
DEFINITION Sequence 16681 from Patent WO0157274.
ACCESSION CQ185285
VERSION CQ185285.1 GI:41180300
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 16681 09-AUG-2001;
Acemica, Inc. (US)

FEATURES
source

1..127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
1.6-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 7

CQ234920
LOCUS
DEFINITION Sequence 21759 from Patent WO0157273.
ACCESSION CQ234920
VERSION CQ234920.1 GI:41218197
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 21759 09-AUG-2001;
Acemica, Inc. (US)

FEATURES
source

1..127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
= 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 8

CQ272476
LOCUS
DEFINITION Sequence 20737 from Patent WO0157277.
ACCESSION CQ272476
VERSION CQ272476.1 GI:41245080
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for

analysis of gene expression in human fetal liver
Patent: WO 0157277-A 20737 09-AUG-2001;
Aeomica, Inc. (US)

JOURNAL
FEATURES
source
Location/Qualifiers

1. .127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL = 4.1-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE 1.00e-65"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 9

CQ310145
LOCUS 127 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21250 from Patent WO0186003.
ACCESSION CQ310145
VERSION CQ310145.1 GI:41270722

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung

JOURNAL Patent: WO 0186003-A 21250 15-NOV-2001;

Aeomica, Inc. (US)

FEATURES

source
1. .127
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL = 2.2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE 1.00e-65"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 10

CQ346752
LOCUS 127 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 20846 from Patent WO0157275.
ACCESSION CQ346752
VERSION CQ346752.1 GI:41295823

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 20846 09-AUG-2001;
Aeomica, Inc. (US)

FEATURES
source
Location/Qualifiers

1. .127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL = 2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE 1.00e-65"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 11

CQ732731/c
LOCUS 387 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 18665 from Patent WO02068579.
ACCESSION CQ732731
VERSION CQ732731.1 GI:42313858

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 18665 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES
source
1. .387
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 300 CTTTCGGCTCTCGGCTGC 283

RESULT 12

CQ099589
LOCUS 587 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 8448 from Patent WO0157272.
ACCESSION CQ099589
VERSION CQ099589.1 GI:41068615

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta


```
JOURNAL Patent: WO 0157272-A 8448 09-AUG-2001;
FEATURES   Aecomica, Inc. (US)
source     1. .587
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
           /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
           1.5"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
    |||||
Db 476 CTTTCGGCTCTCGGCTGC 493

RESULT 13
CQ138575
LOCUS      CQ138575          587 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 8597 from Patent WO0157276.
ACCESSION  CQ138575
VERSION     CQ138575.1 GI:41095941
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human bone marrow
JOURNAL     Patent: WO 0157276-A 8597 09-AUG-2001;
            Aecomica, Inc. (US)
FEATURES    Location/Qualifiers
source      1. .587
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
            = 5.5"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
    |||||
Db 476 CTTTCGGCTCTCGGCTGC 493

RESULT 14
CQ175406
LOCUS      CQ175406          587 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 6802 from Patent WO0157274.
ACCESSION  CQ175406
VERSION     CQ175406.1 GI:41170145
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human heart
JOURNAL     Patent: WO 0157274-A 6802 09-AUG-2001;
            Aecomica, Inc. (US)
FEATURES    Location/Qualifiers
source      1. .587
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
            = 1.9"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
    |||||
Db 476 CTTTCGGCTCTCGGCTGC 493

Search completed: February 4, 2005, 23:30:42
Job time : 432.664 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169a-12

Perfect score: 18

Sequence: 1 ctttcggtctcgctgc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	Az46982 Bcl-Xl mR
2	18	100.0	25	12	ADP17303 Renal cel
3	18	100.0	70	10	ADG89109 Cancer de
4	18	100.0	70	12	ADP27571 Human Bcl
5	18	100.0	127	4	ABA72432 Human foe
6	18	100.0	127	4	AAI52843 Probe #21
7	18	100.0	127	4	ABA38215 Probe #16
8	18	100.0	127	4	AAK47008 Human bon
9	18	100.0	127	4	AAK20855 Human bra
10	18	100.0	127	4	ABA46769 Human liv
11	18	100.0	127	6	ABS21259 Human gen
12	18	100.0	179	12	ACH84269 Human gen
13	18	100.0	299	10	ACD94503 Human col
14	18	100.0	337	10	ADK66037 Standard
15	18	100.0	492	9	ACH46093 Human inf
16	18	100.0	587	4	ABA59891 Human foe
17	18	100.0	587	4	AAI39762 Probe #84
18	18	100.0	587	4	ABA28336 Probe #68
19	18	100.0	587	4	AAK34040 Human bon
20	18	100.0	587	4	AAK08161 Human bra
21	18	100.0	587	4	ABS33839 Human liv

22	18	100.0	587	6	ABS08825	Abs08825 Human gen
23	18	100.0	587	12	ACH70569	Ach70569 Human gen
24	18	100.0	636	4	AAH48169	Aah48169 Mutant bc
25	18	100.0	702	5	AAH43464	Aah43464 cDNA clon
26	18	100.0	702	12	ADM45994	Adm45994 Human apo
27	18	100.0	737	2	AAQ81699	Aaq81699 Human thy
28	18	100.0	737	10	ABZ83507	Abz83507 Toxicolog
29	18	100.0	737	11	ADI32132	Adi32132 Human cDN
30	18	100.0	739	12	ADG65218	Adg65218 Human Bcl
31	18	100.0	747	4	AAF30926	Aaf30926 Human Bcl
32	18	100.0	747	12	ADG65209	Adg65209 Human Bcl
33	18	100.0	926	2	AAQ81698	Aaq81698 Human thy
34	18	100.0	926	2	AAT40079	Aat40079 Bcl-XL ge
35	18	100.0	926	3	AAZ93614	Aaz93614 Bcl-X gen
36	18	100.0	926	4	AAI515189	Aai515189 Human bcl
37	18	100.0	926	4	AAC90810	Aac90810 Human Bcl
38	18	100.0	926	6	ABK84766	Abk84766 Human cDN
39	18	100.0	926	8	ABT16641	Abt16641 Human bcl
40	18	100.0	926	10	ADD56779	Add56779 Human bcl
41	18	100.0	926	10	AAD64187	Aad64187 Human bcl
42	18	100.0	926	11	ADI32104	Adi32104 Human cDN
43	18	100.0	926	12	ADH52630	Adh52630 Human ant
44	18	100.0	926	12	ADO19990	Ado19990 Human PRO
45	18	100.0	926	12	ADP13351	Adp13351 Renal cel

ALIGNMENTS

RESULT 1

AAZ46982

ID AAZ46982 standard; DNA; 18 BP.

AC AAZ46982;

XX

DT 14-APR-2000 (first entry)

XX

DE Bcl-Xl mRNA specific antisense oligo L.

XX

KW Anti-apoptotic protein; bcl-XL; tumour; cancer; epithelial; prostate;

KW lung; bladder; bcl-2; vascular lesion; antisense; ss.

XX

OS Homo sapiens.

XX

FN WO200001393-A2.

XX

PD 13-JAN-2000.

XX

PF 02-JUL-1999; 99WO-US015250.

XX

PR 02-JUL-1998; 98US-00109614.

XX

PA (UYCO) UNIV COLUMBIA NEW YORK.

XX

PI Stein CA;

XX

DR WPI; 2000-137140/12.

XX

PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-

PT XL, useful for reducing bcl-XL production in tumor cells to treat cancer

XX

PS or in vascular cells to promote the regression of vascular lesions.

XX

PS Claim 1; Fig 1; 69pp; English.

XX

CC The invention provides antisense oligonucleotides or their derivatives

CC which reduce or eliminate expression of the anti-apoptotic protein bcl-

CC XL. The oligonucleotides can be introduced into tumour cells to reduce

CC bcl-XL production to treat cancer, especially epithelial cancer, e.g.

CC prostate, lung or bladder cancer. Oligonucleotides comprising one or more

CC bases with a C-5 propynyl pyrimidine modification may especially be used

CC to reduce levels of bcl-2 family proteins (to which bcl-XL belongs) in

CC such treatment. The oligonucleotides can be introduced into vascular

CC cells to reduce bcl-XL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra
CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
CC represent antisense oligos specific for the bcl-X1 mRNA

XX Sequence 18 BP; 0 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
Db 1 CTTTCGGCTCTCGGCTGC 18

RESULT 2

ADP17303/c
ID ADP17303 standard; DNA; 25 BP.

XX AC ADP17303;
XX DT 26-AUG-2004 (first entry)

XX DE Renal cell carcinoma differentially expressed gene probe #3708.

XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.

OS Homo sapiens.

XX WO2004048933-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-US037481.

XX 21-NOV-2002; 2002US-0427982P.

PR 03-APR-2003; 2003US-0459782P.

XX (AMHP) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.

PA (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

PI Sloni DK;

XX WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 4039; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of

CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.

SQ Sequence 25 BP; 8 A; 6 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
Db 23 CTTTCGGCTCTCGGCTGC 6

RESULT 3

ADG89109/c

ID ADG89109 standard; DNA; 70 BP.

XX AC ADG89109;

XX DT 11-MAR-2004 (first entry)

XX DE Cancer detection method related oligonucleotide #57.

XX ss; cancer; gene expression;
KW estrogen receptor-positive invasive breast cancer.

OS Homo sapiens.

PN WO2003078662-A1.

XX 25-SEP-2003.

XX 12-MAR-2003; 2003WO-US007713.

XX 13-MAR-2002; 2002US-0364890P.

PR 18-SEP-2002; 2002US-0412049P.

XX (GENO-) GENOMIC HEALTH INC.

XX Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;

XX WPI; 2003-767536/72.

XX Predicting clinical outcome for a patient diagnosed with cancer comprises
PT determining the expression level of one or more genes, and compared to
PT the amount found in a reference cancer tissue set.

XX Disclosure; SEQ ID NO 57; 198pp; English.

XX The invention relates to a method of predicting clinical outcome for a
CC patient diagnosed with cancer by determining the expression level of one
CC or more genes, or their expression products, selected from p53BP2,
CC cathepsin B, cathepsin L, ki67/MiB1, and thymidine kinase in a cancer
CC tissue obtained from the patient, normalized against control gene(s), and
CC compared to the amount found in a reference cancer tissue set. The
CC specification also discloses an array comprising polynucleotides
CC hybridizing to the following genes: FOXM1, PRAME, Bcl2, STK15, CEGP1, Ki-
CC 67, GSTM1, CA9, PR, BRC3, NME1, SURV, GATA3, TERC, YB-1, DPYD, GSTM3,
CC RPS8KB1, Sro, Chkl, ID1, EstR1, p27, CCNE1, XIAP, Chk2, CDC25B, IGFBP,
CC AK055699, PI3KC2A, TGFB3, BAG1, CYP3A4, EPCAM, VEGFC, p52, HENT1, WISP1,
CC HNF1A, NFKBp65, BRCAC, EGFR, TK1, VDR, Contig51037, pENT1, EPHX1, IFIA,
CC CDH1, HIF1, IGFBP3, CTSS, Her2 and DIABLO, immobilized on a solid
CC surface. The methods are useful for predicting clinical outcome for a
CC patient diagnosed with cancer, classifying cancer, and predicting the
CC likelihood of long-term survival of a breast cancer patient, or a patient
CC diagnosed with invasive breast cancer or with estrogen receptor (ER) -
CC positive invasive breast cancer. This sequence corresponds to an
CC oligonucleotide used in the method of the invention.

XX Sequence 70 BP; 19 A; 18 C; 21 G; 12 T; 0 U; 0 Other;

```
Query Match      100.0%; Score 18; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCGGCTCTCGGCTGC 18
DB 47 CTTTCGGCTCTCGGCTGC 30

RESULT 4
ADP27571/c
ID ADP27571 standard; DNA; 70 BP.
XX
AC ADP27571;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human Bclx DNA used as a cancer prognostic marker SeqID 8.
XX
KW Bclx; human; PCR amplicon; ds; prognostic marker; EGFR;
KW epidermal growth factor receptor; cancer; gene expression profiling;
KW microarray; head and neck cancer; colon cancer; metastatic spread;
KW neoplastic disease.
XX
OS Homo sapiens.
XX
FN WO2004046386-A1.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-US036777.
XX
PR 15-NOV-2002; 2002US-0427090P.
XX
PA (GENO-) GENOMIC HEALTH INC.
XX
PA (VALL-) VALL HEBRON UNIV HOSPITAL.
XX
PI Baker JB, Cronin MT, Shak S, Baselga J;
XX WPI; 2004-420643/39.
XX
PT Prognosing a patient with EGFR-expressing colon cancer comprises
PT subjecting a sample comprising EGFR-expressing cancer cells to
PT quantitative analysis of the expression level of the RNA transcript of at
PT least one gene e.g., CD44v3.
XX
PS Claim 55; SEQ ID NO 8; 113pp; English.
XX
CC This invention relates to a novel method concerning prognostic markers
CC associated with EGFR (epidermal growth factor receptor) positive cancer.
CC Specifically, it refers to a gene expression profiling method that can
CC provide a prediction as to whether a patient is likely to respond well to
CC treatment with an EGFR inhibitor. The present invention describes the
CC quantitative analysis of the expression level of the RNA transcript of at
CC least one gene selected from the group of CD44v3, CD44v6, DR5, GROI,
CC KR17, LAMC2 or their products thereof. It further provides a cDNA
CC microarray containing named genes that represent prognostic transcripts
CC which are useful for determining whether a patient diagnosed with an EGFR
CC -expressing head or neck cancer or colon cancer exhibits elevated or
CC decreased expression levels of these genes compared to normal. As such,
CC these methods are also useful for prognosing or predicting the likelihood
CC of cancer-attributable death or progression, including recurrence and
CC metastatic spread of a neoplastic disease, as well as drug resistance.
CC This polynucleotide sequence is a human PCR amplicon DNA sequence used as
CC a prognostic cancer marker, given in an exemplification of the invention.
XX
SQ Sequence 70 BP; 19 A; 18 C; 21 G; 12 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCGGCTCTCGGCTGC 18
```

```
DB 47 CTTTCGGCTCTCGGCTGC 30

RESULT 5
ABA72432
ID ABA72432 standard; DNA; 127 BP.
XX
AC ABA72432;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #20737.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
FN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human foetal liver.
XX
PS Claim 4; SEQ ID NO 20737; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCGGCTCTCGGCTGC 18
DB 77 CTTTCGGCTCTCGGCTGC 94

RESULT 6
AAI52843
ID AAI52843 standard; DNA; 127 BP.
XX
AC AAI52843;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #21529 used to measure gene expression in human placenta sample.
XX
```

KW Probe: microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder; ss.
 XX

OS Homo sapiens.

PN WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

XX Claim 25; SEQ ID NO 21529; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).

XX The present sequence is one such probe. The probes are useful for

CC producing a microarray for predicting, measuring and displaying gene

CC expression in samples derived from human placenta. The probes are useful

CC for antenatal diagnosis of human genetic disorders

XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 4; Length 127;

XX Best Local Similarity 100.0%; Pred. No. 28;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18

Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 7

ABA38215

ID ABA38215 standard; DNA; 127 BP.

XX ABA38215;

XX 23-JAN-2002 (first entry)

DE Probe #16681 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease; ss.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

XX Claim 25; SEQ ID NO 21529; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).

XX The present sequence is one such probe. The probes are useful for

CC producing a microarray for predicting, measuring and displaying gene

CC expression in samples derived from human placenta. The probes are useful

CC for antenatal diagnosis of human genetic disorders

XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 4; Length 127;

XX Best Local Similarity 100.0%; Pred. No. 28;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18

Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 7

ABA38215

ID ABA38215 standard; DNA; 127 BP.

XX ABA38215;

XX 23-JAN-2002 (first entry)

DE Probe #16681 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease; ss.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT hearts.

XX Claim 4; SEQ ID NO 16681; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart. The

CC present sequence is one such probe. The probes may be used for

CC predicting, measuring and displaying gene expression in samples derived

CC from the human heart via microarrays. By measuring gene expression, the

CC probes are useful for predicting, diagnosing, grading, staging,

CC monitoring and prognosing diseases of the human heart and vascular system

CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and

CC congenital heart disease. Note: The sequence data for this patent did not

CC form part of the printed specification, but was obtained in electronic

CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 4; Length 127;

XX Best Local Similarity 100.0%; Pred. No. 28;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18

Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 8

AAK47008

ID AAK47008 standard; DNA; 127 BP.

XX AAK47008;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 21565.

XX Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing
PI gene expression in human bone marrow.

PS Example 4; SEQ ID NO 21565; 658pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention

SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18

Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 9

AAK20855

ID AAK20855 standard; DNA; 127 BP.

AC AAK20855;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe SEQ ID NO: 20846.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.

XX Homo sapiens.

OS WO200157275-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000667.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human
PI brains.

PS Example 4; SEQ ID NO 20846; 650pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention

SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18

Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 10

ABS46769

ID ABS46769 standard; DNA; 127 BP.

XX AC ABS46769;

XX DT 25-FEB-2003 (first entry)

XX DE Human liver single exon probe, SEQ ID NO 21759.

XX Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.

XX OS Homo sapiens.

XX WO200157273-A2.

XX PN 09-AUG-2001.

XX PD 30-JAN-2001; 2001WO-US000664.

XX PF 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
PI gene expression in human adult liver.

XX Claim 4; SEQ ID NO 21759; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18

Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 11
 ABS21259
 ID ABS21259 standard; DNA; 127 BP.
 XX
 AC ABS21259;
 DT 19-AUG-2002 (first entry)
 XX Human genome-derived single exon probe ORF from lung SEQ ID NO 21250.
 DE Human; db; single exon probe; asthma; lung cancer; COPD; ILD;
 XX chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease; open reading frame; ORF.
 XX Homo sapiens.
 OS
 XX
 XX WO200186003-A2.
 PN
 XX
 PD 15-NOV-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234487P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 DR
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples.
 PT
 XX
 XX Claim 4; SEQ ID NO 21250; 634pp; English.
 PS
 XX The invention relates to a spatially-addressable set of single exon
 XX nucleic acid probes for measuring gene expression in a sample derived
 XX from human lung comprising single exon nucleic acid probes having one of
 XX 12614 nucleic acid sequences mentioned in the specification, or their
 XX complements or the 12387 open reading frames derived from the 12614
 XX probes. Also included are a microarray comprising the novel set of probes
 XX and the novel set of probes which hybridise at high stringency to a nucleic
 XX acid expressed in the human lung; measuring gene expression in a sample
 XX derived from human lung, comprising (a) contacting the array with a
 XX collection of detectably labeled nucleic acids derived from human lung
 XX mRNA, and (b) measuring the label detectably bound to each probe of the
 XX array; identifying exons in a eukaryotic genome, comprising (a)
 XX algorithmically predicting at least one exon from genomic sequences of
 XX the eukaryote; and (b) detecting specific hybridisation of detectably
 XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 XX having a fragment identical to the predicted exon, the probe is included
 XX in the above mentioned microarray; assigning exons to a single gene,
 XX comprising (a) identifying exons from genomic sequence by the method
 XX above and (b) measuring the expression of each of the exons in several
 XX tissues and/or cell types using hybridisation to a single exon
 XX microarrays having a probe with the exon, where a common pattern of
 XX expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberculous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a single exon probe open reading frame of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 18; DB 6; Length 127;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTCGGCTCTCGGCTGC 18
 Db 77 CTTTCGGCTCTCGGCTGC 94
 RESULT 12
 ACH84269/c
 ID ACH84269 standard; DNA; 179 BP.
 XX
 AC ACH84269;
 DT 29-JUL-2004 (first entry)
 XX Human genome derived single exon probe #17464.
 DE Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 KW Homo sapiens.
 OS
 XX US2003194704-A1.
 PN
 XX 16-OCT-2003.
 PD
 XX 03-APR-2002; 2002US-00029386.
 PF
 XX 03-APR-2002; 2002US-00029386.
 PR
 XX (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX Penn SG, Rank DR, Hanzel DK;
 PI WPI; 2004-119264/12.
 XX New human genome-derived single exon nucleic acid probes useful for human
 XX gene expression analysis, for identifying or characterizing alternative
 XX splicing events, for assessing genomic alterations or as tools for
 XX surveying tissues.
 PS Claim 1; SEQ ID NO 17464; 80pp; English.
 XX The invention relates to a nucleic acid probe for measuring human gene
 XX expression, comprising any of the 27,400 fully defined nucleotide
 XX sequences in the specification, or their complements or fragments, and
 XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
 XX fully defined in the specification. The probe is a single exon probe that
 XX hybridises under high stringency conditions to a nucleic acid molecule
 XX expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above). The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 CC
 CC Sequence 179 BP; 37 A; 53 C; 48 G; 41 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 179;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
 Db 71 CTTTCGGCTCTCGGCTGC 54

RESULT 13
 ACD94503/C
 ID ACD94503 standard; cDNA; 299 BP.

AC ACD94503;
 DT 23-SEP-2003 (first entry)
 XX Human colon cancer cell expressed cDNA #2915.

DE Open reading frame detection; genome sequencing; colon cancer;
 KW breast cancer; population genome analysis; genetic shift; cancer;
 KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
 KW agriculture; food crop genome; resistance gene; retrovirus;
 KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
 KW gene; ss.

OS Homo sapiens.
 XX US2002155438-A1.
 XX 24-OCT-2002.

XX 27-SEP-1999; 99US-00406117.
 XX 20-NOV-1998; 98US-00196716.

XX (SIMP// SIMPSON A J G.
 XX (NETO// NETO E D.
 XX (BREN// BRENTANI R R.

XX Simpson AJG, Neto ED, Brentani RR;

DR WPI; 2003-182626/18.

XX Determining open reading frames of genome of an organism e.g. a human
 PT suffering from cancer involves use of single oligonucleotide primer at
 PT low stringency for preparing single-stranded cDNA from mRNA of
 PT individual.

XX Example 9; Page 432; 959pp; English.

XX The invention describes a method of determining open reading frames in
 CC the genome of organism, comprising contacting mRNA from cell of organism
 CC with a single oligonucleotide primer (1) at low stringency, preparing
 CC single-stranded cDNA by reverse transcribing mRNA with (1), amplifying
 CC cDNA, sequencing the product, and repeating the contacting, preparing
 CC and amplifying steps with different primers and sequencing resulting
 CC nucleic acids. The method is useful for: determining that a known
 CC nucleotide sequence from a genome of an organism corresponds to a
 CC nucleotide sequence of an open reading frame; for preparing a contig,
 CC nucleic acid molecule from a genome of an organism; and for sequencing
 CC all or part of a genome of an organism. mRNA is obtained from mammalian
 CC or human cell which is associated with a pathological condition e.g. a
 CC colon cancer or breast cancer cell. The method is useful for analyses of
 CC populations of subjects and can be used to carry out genetic analyses of
 CC large or small populations. Further, it can be used to study living
 CC systems to determine if, e.g. there have been genetic shifts which render
 CC an individual or population more or less likely to be afflicted with
 CC diseases such as cancer, to determine antibiotic resistance or non-
 CC tolerance, and so forth. The method can also be used in the study of
 CC congenital diseases, and the risk of affliction to a fetus, as well as
 CC the study of whether the conditions are likely to be passed to offspring
 CC through ova or sperm. The analyses for pathological conditions can be
 CC carried out in all animals, plants, birds, fish, etc. Using this method,
 CC in the area of agriculture, for example the genomes of food crops can be
 CC studied to determine if resistance genes are present, defects in plant
 CC genomes can also be studied in this way. Similarly, the method permits
 CC determination of the pathogens which integrate into the genome, such as
 CC retroviruses and other integrating viruses such as influenza virus, have
 CC undergone shifts or mutations, which may require different approaches to
 CC therapy. This method is also applied to eukaryotic pathogens, such as
 CC trypanosomes, different types of Plasmodium, etc. The method essentially
 CC eliminates sequencing of non-coding portions. This sequence represents a
 CC polynucleotide isolated from human colon cancer cell cDNA library

XX Sequence 299 BP; 64 A; 95 C; 74 G; 66 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 299;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
 Db 49 CTTTCGGCTCTCGGCTGC 32

RESULT 14
 ADK66037/C
 ID ADK66037 standard; DNA; 337 BP.

AC ADK66037;

XX 06-MAY-2004 (first entry)

XX Standardized polynucleotide system polynucleotide #8.

XX ss; standardized polynucleotide system; medical diagnosis;
 KW functional genomics; sample analysis; pharmacogenomics; sample analysis.
 XX Unidentified.

XX DE10209071-A1.

XX 25-SEP-2003.

XX

```
PF 28-FEB-2002; 2002DE-01009071.
XX
XX 28-FEB-2002; 2002DE-01009071.
XX
XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
XX
XX Koehler T, Rost A;
XX
XX WPI; 2003-732912/70.
XX
XX Standardized polynucleotide system, useful for quantitative, real-time
XX determination of nucleic acid, comprises stabilized standards, primers
XX and probe.
XX
XX Claim 1; Page 7; 38pp; German.
XX
XX The present invention relates to a standardized polynucleotide system,
XX which comprises at least one carrier nucleic acid, at least 3
XX oligonucleotides, as primers and target-specific, fluorescently labeled
XX probe and optionally at least one set of stabilized controls (standard
XX RNA or DNA) of known concentration and instructions. The system comprises
XX any of 20 sets of one control, two primers and one target-specific probe.
XX The standardized polynucleotide system can be used for quantitative, real
XX -time detection of target nucleic acids, especially analysis of genes or
XX gene products, e.g. for individualized medical diagnosis, in veterinary
XX medicine, functional genomics, clinical pharmacology, pharmacogenetics,
XX pharmaceutical testing, analysis of food or environmental samples and
XX also for ultra-sensitive detection of proteins by immuno-PCR. The present
XX sequence is a polynucleotide used in the system of the invention.
XX
XX Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 10; Length 337;
XX Best Local Similarity 100.0%; Pred. No. 29;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CTTTCGGCTCTCGGCTGC 18
XX |||||
XX Db 212 CTTTCGGCTCTCGGCTGC 195
XX
XX RESULT 15
XX ACH46093/C
XX ID ACH46093 standard; cDNA; 492 BP.
XX
XX AC ACH46093;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human infant brain cDNA #156.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
XX
XX US2003073623-A1.
XX
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 33305; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 9; Length 492;
XX Best Local Similarity 100.0%; Pred. No. 30;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CTTTCGGCTCTCGGCTGC 18
XX |||||
XX Db 396 CTTTCGGCTCTCGGCTGC 379
XX
XX Search completed: February 4, 2005, 21:52:44
XX Job time : 233.23 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-12

Perfect score: 18
Sequence: 1 ctttcgctctcgctgc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsl1.*
9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	167	2	BF929309 IL2-NT020
2	18	100.0	216	2	BF806802 PM2-CI011
3	18	100.0	232	2	BF804861 PM2-CI011
C 4	18	100.0	233	1	AI904167 CM-BT043-
5	18	100.0	283	2	BF823588 RCS-RT005
C 6	18	100.0	332	2	AW820481 QV2-ST029
C 7	18	100.0	339	2	BE925384 PMO-AN008
C 8	18	100.0	358	2	AW820530 QV2-ST029
C 9	18	100.0	396	4	EW818649 K-EST0085
10	18	100.0	418	4	BI051278 CM3-GN029
C 11	18	100.0	418	4	BI051278 CM3-GN029
C 12	18	100.0	442	1	AA903741 Ok64a12.8
C 13	18	100.0	447	4	EW818387 K-EST0085
C 14	18	100.0	482	2	BE378810 601237325
C 15	18	100.0	503	4	EW857244 K-EST0141
C 16	18	100.0	516	7	H09884 Ym05067.r1
C 17	18	100.0	522	2	BE395937 601312716
C 18	18	100.0	555	2	BE393580 601310279
C 19	18	100.0	563	2	BE617040 601441454
C 20	18	100.0	579	4	EW741157 K-EST0013
C 21	18	100.0	607	5	HQ36684 hdl3a09.y
C 22	18	100.0	620	4	EW820164 K-EST0088
C 23	18	100.0	652	4	EW043798 603620649
C 24	18	100.0	681	6	CF147016 UI-HF-CBO

C 25	18	100.0	687	2	BE293685
C 26	18	100.0	695	4	BI252492
C 27	18	100.0	699	2	BE870269
C 28	18	100.0	700	4	EG831301
C 29	18	100.0	705	4	EG290422
C 30	18	100.0	714	4	EG470667
C 31	18	100.0	720	6	CD636470
C 32	18	100.0	725	6	CD636468
C 33	18	100.0	728	4	BI696629
C 34	18	100.0	737	4	EG748447
C 35	18	100.0	739	4	EG437506
C 36	18	100.0	765	2	BF569393
C 37	18	100.0	765	2	BE873153
C 38	18	100.0	767	2	BE512918
C 39	18	100.0	782	2	BE249973
C 40	18	100.0	798	5	BQ687097
C 41	18	100.0	798	5	BU528551
C 42	18	100.0	798	7	CK000319
C 43	18	100.0	803	4	EG744242
C 44	18	100.0	808	4	BI222971
C 45	18	100.0	817	5	BQ943707

ALIGNMENTS

RESULT 1
BF929309 167 bp mRNA linear EST 19-JAN-2001
LOCUS IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cdna, mRNA sequence.
DEFINITION BF929309 GI:12327437
ACCESSION
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 167)
AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunsstein,A., deOliveira,P.S., Bucher,F., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc.Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL2&t2=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 167.
Location/Qualifiers
1. 167
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0202"

FEATURES

source
1. 167
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0202"
/notes="Organ: nervous tumor; Vector: puc18; Site: 1: Smal; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 113 CTTTCGGCTCTCGGCTGC 130

RESULT 2

BF806802
LOCUS PM2-CI0111-091100-004-b10 CI0111 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF806802 216 bp mRNA linear EST 12-JAN-2001
PM2-CI0111-091100-004-b10 CI0111 Homo sapiens cDNA, mRNA sequence.
BF806802
VERSION
KEYWORDS
SOURCE
ORGANISM

BF806802 1 GI:12135791
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
COMMENT

CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-CI0111-
091100-004-b10&t3=2000-11-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 216.

FEATURES
source
1..216
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CI0111"
/note="Organ: colon ins; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 100.0%; Score 18; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 113 CTTTCGGCTCTCGGCTGC 130

RESULT 3
BF804861
LOCUS PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF804861 232 bp mRNA linear EST 12-JAN-2001
PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA, mRNA sequence.
BF804861
VERSION
KEYWORDS
SOURCE
ORGANISM

BF804861 1 GI:12133850
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
COMMENT

CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-CI0111-
041100-001-d01&t3=2000-11-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 232.

FEATURES
source
1..232
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CI0111"
/note="Organ: colon ins; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 100.0%; Score 18; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 128 CTTTCGGCTCTCGGCTGC 145

RESULT 4
AI904167
LOCUS CM-BT043-090299-089 BT043 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION

AI904167 233 bp mRNA linear EST 30-MAR-2000
CM-BT043-090299-089 BT043 Homo sapiens cDNA, mRNA sequence.
AI904167

```

VERSION      AI904167.1  GI:6494554
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 233)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT043-089.html
              &t3=090299&t4=1)
              Seq primer: puc 18 forward.
              Location/Qualifiers
                1..233
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /sex="female"
                  /dev stage="Adult"
                  /clone lib="BT043"
                  /note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
                  SmaI; A mini-library was made by cloning products derived
                  from ORESTES PCR (U.S. Letters Patent application No.
                  196,716 - Ludwig Institute for Cancer Research) profiles
                  into the pUC 18 vector. Reverse transcription of tissue
                  mRNA and cDNA amplification were performed under low
                  stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CTTTCGGCTCTCGGCTGC 18
      |||||
Db   49 CTTTCGGCTCTCGGCTGC 32

RESULT 5
LOCUS      BF823588                283 bp    mRNA    linear    EST 13-JAN-2001
DEFINITION RC5-RT0055-221200-011-G02 RT0055 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF823588
VERSION     BF823588.1  GI:12164528
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 283)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT043-089.html
              &t3=090299&t4=1)
              Seq primer: puc 18 forward.
              Location/Qualifiers
                1..233
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /sex="female"
                  /dev stage="Adult"
                  /clone lib="BT043"
                  /note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
                  SmaI; A mini-library was made by cloning products derived
                  from ORESTES PCR (U.S. Letters Patent application No.
                  196,716 - Ludwig Institute for Cancer Research) profiles
                  into the pUC 18 vector. Reverse transcription of tissue
                  mRNA and cDNA amplification were performed under low
                  stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CTTTCGGCTCTCGGCTGC 18
      |||||
Db   49 CTTTCGGCTCTCGGCTGC 32

RESULT 6
LOCUS      AW820481/c              332 bp    mRNA    linear    EST 17-MAY-2000
DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW820481
VERSION     AW820481.1  GI:7913475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 332)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/seq/gethtml.pl?tl=RC5&t2=RC5-RT0055-
              221200-011-G02&t3=2000-12-22&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 283.
              Location/Qualifiers
                1..283
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /dev stage="Adult"
                  /clone lib="RT0055"
                  /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;
                  Site 2: SmaI; A mini-library was made by cloning products
                  derived from ORESTES PCR (U.S. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the pUC 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CTTTCGGCTCTCGGCTGC 18
      |||||
Db   158 CTTTCGGCTCTCGGCTGC 175

RESULT 6
LOCUS      AW820481/c              332 bp    mRNA    linear    EST 17-MAY-2000
DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW820481
VERSION     AW820481.1  GI:7913475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 332)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/seq/gethtml.pl?tl=RC5&t2=RC5-RT0055-
              221200-011-G02&t3=2000-12-22&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 283.
              Location/Qualifiers
                1..283
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /dev stage="Adult"
                  /clone lib="RT0055"
                  /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;
                  Site 2: SmaI; A mini-library was made by cloning products
                  derived from ORESTES PCR (U.S. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the pUC 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CTTTCGGCTCTCGGCTGC 18
      |||||
Db   158 CTTTCGGCTCTCGGCTGC 175

```

```

TITLE
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-
              221200-011-G02&t3=2000-12-22&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 283.
              Location/Qualifiers
                1..283
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /dev stage="Adult"
                  /clone lib="RT0055"
                  /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;
                  Site 2: SmaI; A mini-library was made by cloning products
                  derived from ORESTES PCR (U.S. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the pUC 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CTTTCGGCTCTCGGCTGC 18
      |||||
Db   158 CTTTCGGCTCTCGGCTGC 175

RESULT 6
LOCUS      AW820481/c              332 bp    mRNA    linear    EST 17-MAY-2000
DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW820481
VERSION     AW820481.1  GI:7913475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 332)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-
              221200-011-G02&t3=2000-12-22&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 283.
              Location/Qualifiers
                1..283
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /dev stage="Adult"
                  /clone lib="RT0055"
                  /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;
                  Site 2: SmaI; A mini-library was made by cloning products
                  derived from ORESTES PCR (U.S. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the pUC 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CTTTCGGCTCTCGGCTGC 18
      |||||
Db   158 CTTTCGGCTCTCGGCTGC 175

RESULT 6
LOCUS      AW820481/c              332 bp    mRNA    linear    EST 17-MAY-2000
DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW820481
VERSION     AW820481.1  GI:7913475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 332)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-
              221200-011-G02&t3=2000-12-22&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 283.
              Location/Qualifiers
                1..283
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /dev stage="Adult"
                  /clone lib="RT0055"
                  /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;
                  Site 2: SmaI; A mini-library was made by cloning products
                  derived from ORESTES PCR (U.S. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the pUC 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CTTTCGGCTCTCGGCTGC 18
      |||||
Db   158 CTTTCGGCTCTCGGCTGC 175

```

Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=QV2-ST0298-140>)
200-042-f126t3-2000-02-14&t4=1
Seq primer: puc 18 forward
High quality sequence stop: 332.

FEATURES

source
Location/Qualifiers
1. .332
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ST0298"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 216 CTTTCGGCTCTCGGCTGC 199

RESULT 7

BE925384/c
LOCUS
PMO-AN0087-180800-001-b07 AN0087 Homo sapiens cDNA, mRNA sequence.
DEFINITION
BE925384
VERSION
BE925384.1 GI:10451460
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 339)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=PMO-AN0087-180>)
800-001-b07&t3=2000-08-18&t4=1
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 339.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=QV2-ST0298-140>)
200-042-f126t3-2000-02-14&t4=1
Seq primer: puc 18 forward
High quality sequence stop: 332.

FEATURES

source
Location/Qualifiers
1. .339
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="AN0087"
/note="Organ: amnion normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 56 CTTTCGGCTCTCGGCTGC 39

RESULT 8

AW820530/c
LOCUS
QV2-ST0298-220200-061-d10 ST0298 Homo sapiens cDNA, mRNA sequence.
DEFINITION
AW820530
ACCESSION
AW820530.1 GI:7913524
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 358)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=QV2-ST0298-220>)
200-061-d10&t3=2000-02-22&t4=1
Seq primer: puc 18 forward
High quality sequence start: 44
High quality sequence stop: 358.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=QV2-ST0298-220>)
200-061-d10&t3=2000-02-22&t4=1
Seq primer: puc 18 forward
High quality sequence start: 44
High quality sequence stop: 358.

FEATURES

source
Location/Qualifiers
1. .358
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ST0298"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 230 CTTTCGGCTCTCGGCTGC 213

RESULT 9

BM818649/c

LOCUS BM818649 396 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0085991 S20T665307 Homo sapiens cDNA clone S20T665307-4-F03
5', mRNA sequence.

ACCESSION BM818649

VERSION BM818649.1 GI:19175062

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 396)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsaung@mail.kribb.re.kr

Plate: 4 row: F column: 03

High quality sequence stop: 396.

FEATURES

source

Location/Qualifiers

1..396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-4-F03"
/sex="M"
/lab_host="Top10F"
/clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 249 CTTTCGGCTCTCGGCTGC 232

RESULT 10

BI051278

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 418)

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-

110101-607-f03&t3=2001-01-11&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 3

High quality sequence stop: 418.

Location/Qualifiers

1..418

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="GN0297"

/note="Organ: placenta normal; Vector: puc18; Site 1:

SmaI; Site 2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 418;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18

|||||

Db 110 CTTTCGGCTCTCGGCTGC 127

RESULT 11

BM741875/c

LOCUS

DEFINITION

BM741875

418 bp mRNA linear EST 01-MAR-2002

K-EST0014589 S6SNU620 Homo sapiens cDNA clone S6SNU620-4-C01 5',

mRNA sequence.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BM741875 BM741875.1 GI:19063204 EST. Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 418)
REFERENCE AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 4 row: C column: 01 High quality sequence stop: 418.
FEATURES source	Location/Qualifiers 1..418 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="S6SNU620-4-C01" /sex="F" /tissue_type="Aescites" /cell_type="Scattering floating" /cell_line="SNU-620" /lab_host="Top10F" /clone_lib="S6SNU620" /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
ORIGIN	Query Match 100.0%; Score 18; DB 4; Length 418; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 CTTTCGGCTCTCGGCTGC 18 DB 121 CTTTCGGCTCTCGGCTGC 104 RESULT 12 AA903741 442 bp mRNA linear EST 09-JUN-1998 LOCUS ok64a12.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1518718 3, DEFINITION similar to SW:BCIX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X. ; mRNA sequence. ACCESSION AA903741 GI:3038864 VERSION AA903741.1 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 442) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 536 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham.
FEATURES source	Location/Qualifiers 1..442 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1518718" /tissue_type="pooled germ cell tumors" /lab_host="DH10B" /clone_lib="NCI_CGAP GC4" /note="Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN	Query Match 100.0%; Score 18; DB 1; Length 442; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 CTTTCGGCTCTCGGCTGC 18 DB 354 CTTTCGGCTCTCGGCTGC 371 RESULT 13 BM818387/c LOCUS K-EST0085558 S20T665307 Homo sapiens cDNA clone S20T665307-3-B02 DEFINITION 5', mRNA sequence. ACCESSION BM818387 VERSION BM818387.1 GI:19174800 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 447) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
REFERENCE AUTHORS	21C Frontier Korean EST Project 2001 Unpublished (2002) Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 3 row: B column: 02 High quality sequence stop: 447.
TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 3 row: B column: 02 High quality sequence stop: 447.

FEATURES
source

Location/Qualifiers
1. .447
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-3-B02"
/sex="M"
/lab_host="Top10P"
/clone_lib="S20T665307"
/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 249 CTTTCGGCTCTCGGCTGC 232

RESULT 14

BE378810/c
LOCUS
DEFINITION 601237325P1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609126 5',
482 bp mRNA linear EST 21-JUL-2000

ACCESSION BE378810
VERSION BE378810.1 GI:9324175
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 482)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM263 row: b column: 07
High quality sequence start: 4
High quality sequence stop: 479.
High quality sequence stop: 479.

FEATURES

Location/Qualifiers
1. .482
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3609126"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_44"

source

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 187 CTTTCGGCTCTCGGCTGC 170

RESULT 15

BM857244/c
LOCUS
DEFINITION K-EST0141477 S21SNU520 Homo sapiens cDNA clone S21SNU520-78-F09 5',
503 bp mRNA linear EST 06-MAR-2002

ACCESSION BM857244
VERSION BM857244.1 GI:19213643
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 503)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409

Email: yongsungemail.krrib.re.kr
Plate: 78 row: F column: 09
High quality sequence stop: 503.

FEATURES

Location/Qualifiers
1. .503
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNU520-78-F09"
/sex="F"
/tissue_type="Stomach"
/cell_type="Floating aggregates"
/lab_host="Top10P"
/clone_lib="S21SNU520"
/note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 503;
Best/Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 429 CTTTCGGCTCTCGGCTGC 412

Search completed: February 5, 2005, 08:11:53
Job time : 2147.2 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds
(without alignments)
1967.381 Million cell updates/sec

Title: US-09-753-169A-13
Perfect score: 18
Sequence: 1 aaccagcggtgaagcgt 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pi.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235161
2	18	100.0	18	6	BD235182
3	18	100.0	18	6	BD235183
4	18	100.0	18	6	AR140001
5	18	100.0	127	6	CQ112670
6	18	100.0	127	6	CQ151543
7	18	100.0	127	6	CQ185285
8	18	100.0	127	6	CQ234920
9	18	100.0	127	6	CQ272476
10	18	100.0	127	6	CQ310145
11	18	100.0	127	6	CQ346752
12	18	100.0	387	6	CQ732731
13	18	100.0	587	6	CQ099589
14	18	100.0	587	6	CQ138575
15	18	100.0	587	6	CQ175406
16	18	100.0	587	6	CQ221990
17	18	100.0	587	6	CQ259935
18	18	100.0	587	6	CQ297711
19	18	100.0	587	6	CQ334058

c 20	18	100.0	636	6	BD097037
c 21	18	100.0	702	6	BD084108
c 22	18	100.0	702	6	BD102202
c 23	18	100.0	702	9	BT007208
c 24	18	100.0	702	12	BT008248
c 25	18	100.0	737	6	AR054022
c 26	18	100.0	737	6	AR172595
c 27	18	100.0	737	6	IS2012
c 28	18	100.0	737	6	AR371662
c 29	18	100.0	737	6	AR380913
c 30	18	100.0	737	9	HSBCLXS
c 31	18	100.0	926	6	AR054021
c 32	18	100.0	926	6	AR118504
c 33	18	100.0	926	6	AR124952
c 34	18	100.0	926	6	AR144311
c 35	18	100.0	926	6	AR172594
c 36	18	100.0	926	6	BD243042
c 37	18	100.0	926	6	CQ765842
c 38	18	100.0	926	6	E58777
c 39	18	100.0	926	6	IS2011
c 40	18	100.0	926	6	AR371661
c 41	18	100.0	926	6	AR380885
c 42	18	100.0	926	6	AX839772
c 43	18	100.0	926	6	AX925686
c 44	18	100.0	926	9	HSBCLXL
c 45	18	100.0	1236	6	AX085490

ALIGNMENTS

RESULT 1
LOCUS BD235161 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xl.
ACCESSION BD235161
VERSION BD235161.1 GI:33044931
KEYWORDS JP 2002519048-A/13.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stein, C.A.
TITLE Oligonucleotide inhibitors of bcl-xl
JOURNAL Patent: JP 2002519048-A 13 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT OS Artificial Sequence
PN JP 2002519048-A/13
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN
PC C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC A61K47/42,
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..18 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACCAGCGGTGAAGCGT 18
|||||


```

REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human placenta
JOURNAL      Patent: WO 0157272-A 21529 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..127
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
              1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
              AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACACGCGGTTGAAGCGT 18
        |||||
Db      51 AACACGCGGTTGAAGCGT 68

RESULT 6
CQ151543
LOCUS      CQ151543      127 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 21565 from Patent WO0157276.
ACCESSION  CQ151543
VERSION     CQ151543.1 GI:41158893
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human bone marrow
JOURNAL      Patent: WO 0157276-A 21565 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..127
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
              = 5.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
              HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACACGCGGTTGAAGCGT 18
        |||||
Db      51 AACACGCGGTTGAAGCGT 68

RESULT 7
CQ185285
LOCUS      CQ185285      127 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 16681 from Patent WO0157274.
ACCESSION  CQ185285
VERSION     CQ185285.1 GI:41180300
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human placenta
JOURNAL      Patent: WO 0157272-A 21529 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..127
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
              1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
              AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACACGCGGTTGAAGCGT 18
        |||||
Db      51 AACACGCGGTTGAAGCGT 68

RESULT 8
CQ234920
LOCUS      CQ234920      127 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 21759 from Patent WO0157273.
ACCESSION  CQ234920
VERSION     CQ234920.1 GI:41218197
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
              3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
              60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
              August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
              (03.10.00)<150> US 60/236,359<151> 27 September 2000
              (27.09.00)<150> US 60/234,687<151> 21 September 2000
              (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
              Molecular Dynamics Sequence Listing Engine
              Patent: WO 0157273-A 21759 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..127
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
              = 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
              HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACACGCGGTTGAAGCGT 18
        |||||
Db      51 AACACGCGGTTGAAGCGT 68

RESULT 9
CQ185285
LOCUS      CQ185285      127 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 16681 from Patent WO0157274.
ACCESSION  CQ185285
VERSION     CQ185285.1 GI:41180300
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human placenta
JOURNAL      Patent: WO 0157272-A 21529 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..127
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
              1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
              AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACACGCGGTTGAAGCGT 18
        |||||
Db      51 AACACGCGGTTGAAGCGT 68

```

```

REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human heart
JOURNAL      Patent: WO 0157274-A 16681 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..127
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
              1.6-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
              AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACACGCGGTTGAAGCGT 18
        |||||
Db      51 AACACGCGGTTGAAGCGT 68

RESULT 8
CQ234920
LOCUS      CQ234920      127 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 21759 from Patent WO0157273.
ACCESSION  CQ234920
VERSION     CQ234920.1 GI:41218197
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
              3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
              60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
              August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
              (03.10.00)<150> US 60/236,359<151> 27 September 2000
              (27.09.00)<150> US 60/234,687<151> 21 September 2000
              (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
              Molecular Dynamics Sequence Listing Engine
              Patent: WO 0157273-A 21759 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..127
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
              = 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
              HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACACGCGGTTGAAGCGT 18
        |||||
Db      51 AACACGCGGTTGAAGCGT 68

RESULT 9
CQ185285
LOCUS      CQ185285      127 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 16681 from Patent WO0157274.
ACCESSION  CQ185285
VERSION     CQ185285.1 GI:41180300
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human placenta
JOURNAL      Patent: WO 0157272-A 21529 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..127
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
              1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
              AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACACGCGGTTGAAGCGT 18
        |||||
Db      51 AACACGCGGTTGAAGCGT 68

```

```

CQ272476
LOCUS       CQ272476               127 bp    DNA          linear          PAT 23-JAN-2004
DEFINITION   Sequence 20737 from Patent WO0157277.
ACCESSION    CQ272476
VERSION      CQ272476.1  GI:41245080
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 20737 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
                = 4.1-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
                HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
                1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAGCGGTTGAAGCGT 18
    |||||||
Db 51 AACCAGCGGTTGAAGCGT 68

RESULT 10
CQ310145
LOCUS       CQ310145               127 bp    DNA          linear          PAT 23-JAN-2004
DEFINITION   Sequence 21250 from Patent WO0186003.
ACCESSION    CQ310145
VERSION      CQ310145.1  GI:41270722
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human lung
JOURNAL      Patent: WO 0186003-A 21250 15-NOV-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
                2.2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
                AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
                1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAGCGGTTGAAGCGT 18
    |||||||
Db 51 AACCAGCGGTTGAAGCGT 68

CQ272476
LOCUS       CQ272476               127 bp    DNA          linear          PAT 23-JAN-2004
DEFINITION   Sequence 20737 from Patent WO0157277.
ACCESSION    CQ272476
VERSION      CQ272476.1  GI:41245080
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 20737 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
                = 4.1-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
                HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
                1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAGCGGTTGAAGCGT 18
    |||||||
Db 51 AACCAGCGGTTGAAGCGT 68

CQ310145
LOCUS       CQ310145               127 bp    DNA          linear          PAT 23-JAN-2004
DEFINITION   Sequence 21250 from Patent WO0186003.
ACCESSION    CQ310145
VERSION      CQ310145.1  GI:41270722
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human lung
JOURNAL      Patent: WO 0186003-A 21250 15-NOV-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
                2.2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
                AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
                1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAGCGGTTGAAGCGT 18
    |||||||
Db 51 AACCAGCGGTTGAAGCGT 68

CQ346752
LOCUS       CQ346752               127 bp    DNA          linear          PAT 23-JAN-2004
DEFINITION   Sequence 20846 from Patent WO0157275.
ACCESSION    CQ346752
VERSION      CQ346752.1  GI:41295823
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human brain
JOURNAL      Patent: WO 0157275-A 20846 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
                2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
                AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
                1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAGCGGTTGAAGCGT 18
    |||||||
Db 51 AACCAGCGGTTGAAGCGT 68

CQ732731
LOCUS       CQ732731               387 bp    DNA          linear          PAT 03-FEB-2004
DEFINITION   Sequence 18665 from Patent WO02068579.
ACCESSION    CQ732731
VERSION      CQ732731.1  GI:42313858
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE        Kits, such as nucleic acid arrays, comprising a majority of
              humanexons or transcripts, for detecting expression and other uses
              thereof
JOURNAL      Patent: WO 02068579-A 18665 06-SEP-2002;
              PE Corporation (NY) (US)
FEATURES     Location/Qualifiers
              source
                1..387
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAGCGGTTGAAGCGT 18
    |||||||
Db 326 AACCAGCGGTTGAAGCGT 309

RESULT 11
CQ346752
LOCUS       CQ346752               127 bp    DNA          linear          PAT 23-JAN-2004
DEFINITION   Sequence 20846 from Patent WO0157275.
ACCESSION    CQ346752
VERSION      CQ346752.1  GI:41295823
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human brain
JOURNAL      Patent: WO 0157275-A 20846 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
                2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
                AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
                1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAGCGGTTGAAGCGT 18
    |||||||
Db 51 AACCAGCGGTTGAAGCGT 68

CQ732731
LOCUS       CQ732731               387 bp    DNA          linear          PAT 03-FEB-2004
DEFINITION   Sequence 18665 from Patent WO02068579.
ACCESSION    CQ732731
VERSION      CQ732731.1  GI:42313858
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE        Kits, such as nucleic acid arrays, comprising a majority of
              humanexons or transcripts, for detecting expression and other uses
              thereof
JOURNAL      Patent: WO 02068579-A 18665 06-SEP-2002;
              PE Corporation (NY) (US)
FEATURES     Location/Qualifiers
              source
                1..387
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAGCGGTTGAAGCGT 18
    |||||||
Db 326 AACCAGCGGTTGAAGCGT 309

RESULT 13
CQ099589

```

```

LOCUS       CQ099589               587 bp    DNA    linear    PAT 21-JAN-2004
DEFINITION   Sequence 8448 from Patent WO0157272.
ACCESSION    CQ099589
VERSION      CQ099589.1   GI:41068615
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human placenta
JOURNAL      Patent: WO 0157272-A 8448 09-AUG-2001;
              Acomica, Inc. (US)
FEATURES     source
              1..587
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
              1.5"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACACGCGGTTGAAGCGT 18
        |||||
Db      450 AACACGCGGTTGAAGCGT 467

RESULT 14
LOCUS       CQ138575               587 bp    DNA    linear    PAT 21-JAN-2004
DEFINITION   Sequence 8597 from Patent WO0157276.
ACCESSION    CQ138575
VERSION      CQ138575.1   GI:41095941
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human bone marrow
JOURNAL      Patent: WO 0157276-A 8597 09-AUG-2001;
              Acomica, Inc. (US)
FEATURES     source
              1..587
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
              = 5.5"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACACGCGGTTGAAGCGT 18
        |||||
Db      450 AACACGCGGTTGAAGCGT 467

RESULT 15
LOCUS       CQ175406               587 bp    DNA    linear    PAT 21-JAN-2004
DEFINITION   Sequence 6802 from Patent WO0157274.
ACCESSION    CQ175406

```

VERSION
KEYWORDS
SOURCE
ORGANISM

CQ175406.1 GI:41170145

Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

1..587

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.6"

ORIGIN

Query Match

Best Local Similarity

Matches

18; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy

1 AACACGCGGTTGAAGCGT 18

|||||

Db

450 AACACGCGGTTGAAGCGT 467

Search completed: February 4, 2005, 23:30:42

Job time : 432.664 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds
(without alignments)
406.880 Million cell updates/sec

Title: US-09-753-169A-13
Perfect score: 18
Sequence: 1 aaccagcggttgagcgt 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_238Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	AZ46983 Bcl-Xl MR
2	18	100.0	87	4	Aah19915 Single SN
3	18	100.0	127	4	Aba72432 Human foe
4	18	100.0	127	4	Aai52843 Probe #21
5	18	100.0	127	4	Aba38215 Probe #16
6	18	100.0	127	4	Aak47008 Human bon
7	18	100.0	127	4	Aak20855 Human bra
8	18	100.0	127	4	Abs46769 Human liv
9	18	100.0	127	6	ABs21259 Human gen
10	18	100.0	179	12	ACH84269 Human gen
11	18	100.0	299	10	ACD94503 Human col
12	18	100.0	337	10	ADK66037 Standardi
13	18	100.0	492	9	ACH46093 Human inf
14	18	100.0	587	4	ABA59891 Human foe
15	18	100.0	587	4	AAI39762 Probe #84
16	18	100.0	587	4	ABA28336 Probe #68
17	18	100.0	587	4	AAK34040 Human bon
18	18	100.0	587	4	AAK08161 Human bra
19	18	100.0	587	4	ABS33839 Human liv
20	18	100.0	587	6	ABS08825 Human gen
21	18	100.0	587	12	ACH70569 Human gen

C	22	18	100.0	636	4	AAH48169	Aah48169 Mutant bc
C	23	18	100.0	702	5	AAH43464	Aah43464 cDNA clon
C	24	18	100.0	702	12	ADM45994	Adm45994 Human apo
C	25	18	100.0	737	2	AAQ81699	Aaq81699 Human thy
C	26	18	100.0	737	10	ABZ83507	Abz83507 Toxicolog
C	27	18	100.0	737	11	ADI32132	Adi32132 Human CDN
C	28	18	100.0	926	2	AAQ81698	Aaq81698 Human thy
C	29	18	100.0	926	2	AAT40079	Aat40079 Bcl-XL ge
C	30	18	100.0	926	3	AAZ93614	Aaz93614 Bcl-x gen
C	31	18	100.0	926	4	AAZ93614	Aaz93614 Bcl-x gen
C	32	18	100.0	926	4	AAC90810	Aac90810 Human bcl
C	33	18	100.0	926	6	ABK84766	Abk84766 Human CDN
C	34	18	100.0	926	8	ABT16641	Abt16641 Human bcl
C	35	18	100.0	926	10	ADD56779	Add56779 Human bcl
C	36	18	100.0	926	10	AAD64187	Aad64187 Human bcl
C	37	18	100.0	926	11	ADI32104	Adi32104 Human CDN
C	38	18	100.0	926	12	ADH52630	Adh52630 Human ant
C	39	18	100.0	926	12	ADO19990	Ado19990 Human PRO
C	40	18	100.0	926	12	ADF13351	Adf13351 Renal cel
C	41	18	100.0	1236	5	AAS00247	Aas00247 Bcl-XI-DT
C	42	18	100.0	2386	10	ADG89403	Adg89403 Cancer de
C	43	18	100.0	2386	12	ADN04260	Adn04260 Antipsori
C	44	18	100.0	2575	12	ADO19866	Ado19866 Human PRO
C	45	18	100.0	7372	2	AAZ33182	Aaz33182 Base sequ

ALIGNMENTS

RESULT 1
AAZ46983
ID AAZ46983 standard; DNA; 18 BP.
XX
AC AAZ46983;
XX
DT 14-APR-2000 (first entry)
XX
DE Bcl-Xl mRNA specific antisense oligo M.
XX
KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.
XX
OS Homo sapiens.
XX
PN WC200001393-A2.
XX
PD 13-JAN-2000.
XX
PF 02-JUL-1999; 99WO-US015250.
XX
PR 02-JUL-1998; 98US-00109614.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
Stein CA;
WPI; 2000-137140/12.
New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English.

The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra
 CC meso-(4-methylpyridyl))porphine and/or tetra meso-(anilinium)porphine; in
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
 CC represent antisense oligos specific for the bcl-XL mRNA

XX Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGGTTGAAGCGT 18
 |||||
 Db 1 AACACGCGGTTGAAGCGT 18

RESULT 2
 AAH1915
 ID AAH1915 standard; DNA; 87 BP.

XX AC AAH1915;
 DT 06-AUG-2001 (first entry)
 XX Single SNAP primer SPAS-BCL-1001 directed toward bcl-xS and bcl-xL.
 DE Self-priming nucleic acid polymerase; SNAP; primer; amplification; BCL;
 XX bcl-xS; bcl-xL; human; ss.
 KW Homo sapiens.
 OS US6207424-B1.
 XX 27-MAR-2001.

XX 23-NOV-1999; 99US-00447942.
 XX 23-NOV-1999; 99US-00447942.
 XX (MAXI-) MAXIM BIOTECH INC.
 XX Chou Q, Maa J, Chang C;
 XX WPI; 2001-298942/31.

XX New self-priming nucleic acid polymerase primer for copying target
 PT nucleic acid, contains (anti) sense target specific and non-target
 PT (anti)sense primer binding domains.
 XX Claim 45; Col 18; 20pp; English.
 PS The present invention describes a self-priming nucleic acid polymerase
 CC (SNAP) primer (I) for copying a target nucleic acid (TNA) comprising,
 CC from 3'-5', a sense, target-specific binding domain (TBD), a non-target,
 CC antisense primer binding domain (PBD), non-target, sense PBD and an
 CC antisense TBD. SNAP primers are useful for copying a target nucleic acid
 CC or a mixture of at least two different target nucleic acids. Methods
 CC comprising SNAPS are less likely to produce variable and erroneous
 CC signals in multiplex assays. The present sequence represents a
 CC specifically claimed single SNAP primer designated SPAS-BCL-1001, which
 CC is directed toward bcl-xS and bcl-xL

XX Sequence 87 BP; 19 A; 26 C; 24 G; 18 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 87;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGGTTGAAGCGT 18
 |||||
 Db 70 AACACGCGGTTGAAGCGT 87

RESULT 3
 ABA72432
 ID ABA72432 standard; DNA; 127 BP.
 XX AC ABA72432;

XX 01-FEB-2002 (first entry)
 DT Human foetal liver single exon nucleic acid probe #20737.
 DE Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 KW Homo sapiens.
 OS WO200157277-A2.
 XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX Claim 4; SEQ ID NO 20737; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 127;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGGTTGAAGCGT 18
 |||||
 Db 51 AACACGCGGTTGAAGCGT 68

RESULT 4
 AAI52843
 ID AAI52843 standard; DNA; 127 BP.

XX AC AAI52843;
 DT 17-OCT-2001 (first entry)
 XX Probe #21529 used to measure gene expression in human placenta sample.
 DE Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder; ss.
 XX Homo sapiens.
 OS

```
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PT WPI; 2001-488897/53.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human placenta.
XX PS Claim 25; SEQ ID NO 21529; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP).
XX CC The present sequence is one such probe. The probes are useful for
XX CC producing a microarray for predicting, measuring and displaying gene
XX CC expression in samples derived from human placenta. The probes are useful
XX CC for antenatal diagnosis of human genetic disorders
XX SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. NO. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGGTTGAAGCGT 18
Db 51 AACACGCGGTTGAAGCGT 68

RESULT 5
ABA38215
ID ABA38215 standard; DNA; 127 BP.
XX AC ABA38215;
XX DT 23-JAN-2002 (first entry)
XX DE Probe #16681 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PT WPI; 2001-488897/53.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 21565; 658pp + Sequence Listing; English.

Query Match 100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. NO. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGGTTGAAGCGT 18
Db 51 AACACGCGGTTGAAGCGT 68

RESULT 6
AAK47008
ID AAK47008 standard; DNA; 127 BP.
XX AC AAK47008;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 21565.
XX DE Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PT WPI; 2001-488897/53.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 21565; 658pp + Sequence Listing; English.
```

XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGTTGAAGCGT 18
Db 51 AACACGCGTTGAAGCGT 68

RESULT 7
AAK20855
ID AAK20855 standard; DNA; 127 BP.
XX AC
XX AAK20855;
XX
XX 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe SEQ ID NO: 20846.
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX ss.
XX Homo sapiens.
XX WO200157275-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000667.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX Example 4; SEQ ID NO 20846; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGTTGAAGCGT 18
Db 51 AACACGCGTTGAAGCGT 68

RESULT 8
ABS46769
ID ABS46769 standard; DNA; 127 BP.
XX AC
XX ABS46769;
XX 25-FEB-2003 (first entry)
XX Human liver single exon probe, SEQ ID No 21759.
XX Human; single exon nucleic acid probe; liver; cirrhosis;
XX hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
XX coronary heart disease; ss.
XX Homo sapiens.
XX WO200157273-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000664.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX Claim 4; SEQ ID NO 21759; 658pp; English.
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABS25011-ABS51005 represent human
XX liver single exon nucleic acid probes of the invention. Note: The
XX sequence information for this patent does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGTTGAAGCGT 18
Db 51 AACACGCGTTGAAGCGT 68

RESULT 9
ID ABS21259 standard; DNA; 127 BP.
AC ABS21259;
XX
XX 19-AUG-2002 (first entry)
XX Human genome-derived single exon probe ORF from lung SEQ ID NO 21250.
DE Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
XX Homo sapiens.
XX WO200186003-A2.
XX
XX 15-NOV-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 4; SEQ ID NO 21250; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridize at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridization of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridization to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human

lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCCAGCGTTGAAGCGT 18
Db 51 AACCCAGCGTTGAAGCGT 68

RESULT 10
ACH84269/c
ID ACH84269 standard; DNA; 179 BP.
XX
XX ACH84269;
XX 29-JUL-2004 (first entry)
XX Human genome derived single exon probe #17464.
XX Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
XX Homo sapiens.
XX US2003194704-A1.
XX 16-OCT-2003.
XX 03-APR-2002; 2002US-00029386.
XX 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.
XX Claim 1; SEQ ID NO 17464; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single

PA (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
XX Koehler T, Rost A;
XX WPI; 2003-732912/70.
DR Standardized polynucleotide system, useful for quantitative, real-time
XX determination of nucleic acid, comprises stabilized standards, primers
PT and probe.
XX
PS Claim 1; Page 7; 38pp; German.
XX
CC The present invention relates to a standardized polynucleotide system,
CC which comprises at least one carrier nucleic acid, at least 3
CC oligonucleotides, as primers and target-specific, fluorescently labeled
CC probe and optionally at least one set of stabilized controls (standard
CC RNA or DNA) of known concentration and instructions. The system comprises
CC any of 20 sets of one control, two primers and one target-specific probe.
CC The standardized polynucleotide system can be used for quantitative, real
CC -time detection of target nucleic acids, especially analysis of genes or
CC gene products, e.g. for individualized medical diagnosis, in veterinary
CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,
CC pharmaceutical testing, analysis of food or environmental samples and
CC also for ultra-sensitive detection of proteins by immuno-PCR. The present
CC sequence is a polynucleotide used in the system of the invention.
XX
SQ Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 337;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAGCGT 18
|||||
DB 238 AACACGCGTTGAGCGT 221

RESULT 13
ACH46093/c
ID ACH46093 standard; cDNA; 492 BP.
XX
AC ACH46093;
XX
DT 13-OCT-2003 (first entry)
DE Human infant brain cDNA #156.
XX
DE Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
FN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
DR New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating

antisense DNA or RNA.
Claim 1; SEQ ID NO 33305; 4pp; English.
The invention relates to an isolated polynucleotide comprising any one of
38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
determined by the technique of SBH (sequencing by hybridisation). Also
included is a purified polypeptide comprising a sequence corresponding to
a reading frame of the novel polynucleotide. The nucleic acid sequences
are useful in diagnostics as expressed sequence tags (EST) for
identifying expressed genes or for physical mapping of the human genome,
in forensics, in assessing biodiversity, or in identifying mutations
responsible for genetic disorders and other traits. The nucleotide
sequences are also useful as hybridisation probes, as oligomers for PCR,
for chromosome and gene mapping, in the recombinant production of
protein, or in generating antisense DNA or RNA. The purified polypeptide
is useful for generating antibodies specific for it. The present sequence
is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
for this patent did not form part of the printed specification, but was
obtained in electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html?DocID=20030073623
SQ Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 9; Length 492;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAGCGT 18
|||||
DB 422 AACACGCGTTGAGCGT 405

RESULT 14
ABA59891
ID ABA59891 standard; DNA; 587 BP.
XX
AC ABA59891;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #8196.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
FN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234587P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
DR Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 1; SEQ ID NO 8196; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGTTGAAGCGT 18
| | | | | | | | | | | | | | | | | |
Db 450 AACACGCGTTGAAGCGT 467

RESULT 15

AAI39762
ID AAI39762 standard; DNA; 587 BP.

XX
AC AAI39762;

DT 17-OCT-2001 (first entry)

DE Probe #8448 used to measure gene expression in human placenta sample.

KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.

XX Homo sapiens.

PN WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.

XX Claim 25; SEQ ID NO 8448; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders

XX Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;

Qy 1 AACACGCGTTGAAGCGT 18
| | | | | | | | | | | | | | | | | |

Db 450 AACACGCGTTGAAGCGT 467

Search completed: February 4, 2005, 21:52:44
Job time : 232.23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds
(without alignments)
305.616 Million cell updates/sec

Title: US-09-753-169A-13
Perfect score: 18
Sequence: 1 aaccagcggttgagcgt 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	140	BF948716	BF948716 CM2-NN115
2	18	100.0	154	AW849455	AW849455 IL3-CT021
3	18	100.0	167	BF929109	BF929109 IL2-NT020
4	18	100.0	194	BF880488	BF880488 QV3-ET017
5	18	100.0	216	BF806802	BF806802 PM2-CI011
6	18	100.0	232	BF804861	BF804861 PM2-CI011
7	18	100.0	233	AI904167	AI904167 CM-BT043
8	18	100.0	283	BF823588	BF823588 RC5-RT005
9	18	100.0	332	AW820481	AW820481 QV2-ST029
10	18	100.0	339	BE925384	BE925384 PM0-AN008
11	18	100.0	358	AW820530	AW820530 QV2-ST029
12	18	100.0	396	AW818649	AW818649 K-EST0085
13	18	100.0	418	BI051278	BI051278 CM3-GN029
14	18	100.0	418	BM741875	BM741875 K-EST0014
15	18	100.0	437	W01420	W01420 za73d06.x1
16	18	100.0	442	AA903741	AA903741 ok64a12.s
17	18	100.0	447	AW818387	AW818387 K-EST0085
18	18	100.0	482	BE378810	BE378810 601237325
19	18	100.0	486	AW814883	AW814883 MR1-ST020
20	18	100.0	503	AW857244	AW857244 K-EST0141
21	18	100.0	516	H09884	H09884 ym05b07.x1
22	18	100.0	522	BE395937	BE395937 601312716
23	18	100.0	528	CB118773	CB118773 K-EST0165
24	18	100.0	555	BE393580	BE393580 601310279

25	18	100.0	559	1	AI133331	AI133331 HA1935 Hu
26	18	100.0	563	2	BE617040	BE617040 601441454
27	18	100.0	579	4	BM741157	BM741157 K-EST0013
28	18	100.0	607	5	BO636684	BO636684 hdl3a09.Y
29	18	100.0	620	4	BM820164	BM820164 K-EST0088
30	18	100.0	652	4	BM043798	BM043798 603620649
31	18	100.0	681	6	CF147016	CF147016 UI-HF-C80
32	18	100.0	687	2	BE293685	BE293685 601186941
33	18	100.0	695	4	BI252492	BI252492 602952957
34	18	100.0	697	4	BI457116	BI457116 603185360
35	18	100.0	699	2	BE870269	BE870269 601447403
36	18	100.0	700	4	EG831301	EG831301 602766132
37	18	100.0	705	4	EG290422	EG290422 602388270
38	18	100.0	714	4	EG470667	EG470667 602511594
39	18	100.0	720	6	CD636470	CD636470 56049223J
40	18	100.0	725	6	CD636468	CD636468 56049107J
41	18	100.0	728	4	EG169629	EG169629 602312189
42	18	100.0	737	4	EG748447	EG748447 602706419
43	18	100.0	739	4	EG437506	EG437506 602489238
44	18	100.0	765	2	BF569393	BF569393 602185659
45	18	100.0	765	2	BE873153	BE873153 601451667

ALIGNMENTS

RESULT 1
BF948716
LOCUS BF948716 140 bp mRNA linear EST 22-JAN-2001
DEFINITION CM2-NN1152-311000-454-b02 NN1152 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF948716
VERSION BF948716.1 GI:12365991
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 140)
AUTHORS Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202863
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 140.

FEATURES
source

1. 140
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1152"

/notes="Organ: nervous normal; Vector: puc18; Site: 1: SmaI; Site_2: SmaI; A mini-library was made by cloning products"

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18

DB 104 AACACGCGTTGAAGCGT 121

RESULT 2
AW849455
LOCUS
DEFINITION IL3-CT0215-170300-093-F10_1 CT0215 Homo sapiens cDNA, mRNA
sequence.
ACCESSION
AW849455
VERSION
AW849455.1 GI:7945076
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
1 (bases 1 to 154)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=IL3-CT0215-170300-093-F10.1&t3=2000-03-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 52.

FEATURES
source
1..154
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0215"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 100.0%; Score 18; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
BF929309
LOCUS
DEFINITION IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF929309
VERSION
BF929309.1 GI:12327437
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
1 (bases 1 to 167)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 167.

QY 1 AACACGCGTTGAAGCGT 18

DB 121 AACACGCGTTGAAGCGT 138

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18

DB 87 AACACGCGTTGAAGCGT 104

RESULT 4
BF880488
LOCUS
DEFINITION QV3-ET0175-011200-514-a04 ET0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF880488

REFERENCE
1 (bases 1 to 167)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL2&t2=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 167.

FEATURES
source
1..167
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0202"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 100.0%; Score 18; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18

DB 87 AACACGCGTTGAAGCGT 104

RESULT 4
BF880488
LOCUS
DEFINITION QV3-ET0175-011200-514-a04 ET0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF880488

REFERENCE
1 (bases 1 to 167)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL2&t2=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 167.

```

VERSION      BF80488.1  GI:12270718
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 194)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0175-
              011200-514-a04&t3=2000-12-01&t4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 17
              High quality sequence stop: 194.
              Location/Qualifiers
FEATURES     source
              1..194
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /dev_stage="Adult"
               /clone_lib="ET0175"
               /note="Organ: lung tumor; Vector: puc18; Site:1: SmaI;
               Site_2: SmaI; A mini-library was made by cloning products
               derived from ORESTES PCR (U.S. Letters Patent application
               No. 196,716 - Ludwig Institute for Cancer Research)
               profiles into the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed under
               low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACACGCGGTGAAGCGT 18
        |||||
Db      146 AACACGCGGTGAAGCGT 163

RESULT 5
BF806802
LOCUS      BF806802
DEFINITION PM2-CI0111-091100-004-B10 CI0111 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF806802
VERSION     BF806802.1  GI:12135791
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 216)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0175-
              011200-514-a04&t3=2000-12-01&t4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 17
              High quality sequence stop: 194.
              Location/Qualifiers
FEATURES     source
              1..216
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /dev_stage="Adult"
               /clone_lib="CI0111"
               /note="Organ: colon ins; Vector: puc18; Site:1: SmaI;
               Site_2: SmaI; A mini-library was made by cloning products
               derived from ORESTES PCR (U.S. Letters Patent application
               No. 196,716 - Ludwig Institute for Cancer Research)
               profiles into the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed under
               low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACACGCGGTGAAGCGT 18
        |||||
Db      86  AACACGCGGTGAAGCGT 103

RESULT 6
BF804861
LOCUS      BF804861
DEFINITION PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF804861
VERSION     BF804861.1  GI:12133850
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 232)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics

```

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-041100-001-001&t3=2000-11-04&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 13
 High quality sequence stop: 232.

FEATURES

source

Location/Qualifiers
 1. .232
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="CI0111"
 /note="Organ: colon_ins; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGCGGTGAAGCGT 18
 |||||
 Db 102 AACGAGCGGTGAAGCGT 119

RESULT 7

AI904167/c
 LOCUS AI904167 233 bp mRNA linear EST 30-MAR-2000
 DEFINITION CW-BT043-090299-089 BT043 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AI904167
 VERSION AI904167.1 GI:6494554
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS
 1 (bases 1 to 233)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED

10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT043-089.html&t3=090299&t4=1>)

Seq primer: puc 18 forward.
 Location/Qualifiers
 1. .233
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="Adult"
 /clone_lib="BT043"
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGCGGTGAAGCGT 18
 |||||
 Db 75 AACGAGCGGTGAAGCGT 58

RESULT 8

BF823588
 LOCUS BF823588 283 bp mRNA linear EST 13-JAN-2001
 DEFINITION RC5-RT0055-221200-011-G02 RT0055 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF823588
 VERSION BF823588.1 GI:12164528
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS
 1 (bases 1 to 283)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED

10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-221200-011-G02&t3=2000-12-22&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 283.

FEATURES

source

Location/Qualifiers
 1. .283
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="RT0055"
 /note="Organ: kidney tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGTTGAAGCGT 18
|||||

Db 132 AACACGCGTTGAAGCGT 149
|||||

RESULT 9

AW820481/c
LOCUS
DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence. EST 17-MAY-2000
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=QV2-ST0298-140200-042-f12&t3=2000-02-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
Location/Qualifiers

FEATURES

source

1. 332
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ST0298"

/note="Organ: stomach; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGTTGAAGCGT 18
|||||

Db 242 AACACGCGTTGAAGCGT 225
|||||

RESULT 10

BE925384/c
LOCUS
DEFINITION PMO-AN0087-180800-001-b07 AN0087 Homo sapiens cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=PMO-AN0087-180800-001-b07&t3=2000-08-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 339.
Location/Qualifiers

FEATURES

source

1. 339
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="AN0087"
/note="Organ: amnion normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGTTGAAGCGT 18
|||||

Db 81 AACACGCGTTGAAGCGT 64
|||||

RESULT 11

AW820530/c
LOCUS
DEFINITION QV2-ST0298-220200-061-d10 ST0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION

```

VERSION      AW820530.1  GI:7913524
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens

REFERENCE
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.

TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags

JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=QV2-ST0298-220
              200-061-d10&t3=2000-02-22&t4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 44
              High quality sequence stop: 358.

FEATURES
source
    1..358
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone_lib="ST0298"
        /dev_stage="Adult"
        /notes="Organ: stomach; Vector: puc18; Site 1: SmaI;
        Site 2: SmaI; A mini-library was made by cloning products
        derived from ORESTES PCR (U.S. Letters Patent application
        No. 196,716 - Ludwig Institute for Cancer Research)
        profiles into the pUC 18 vector. Reverse transcription of
        tissue mRNA and cDNA amplification were performed under
        low stringency conditions."

ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGGTTGAAGCGT 18
    |||||
Db 256 AACACGCGGTTGAAGCGT 239

RESULT 12
BM818649/c
LOCUS          BM818649          396 bp      mRNA      linear      EST 06-MAR-2002
DEFINITION    K-EST0085991 S20T665307 Homo sapiens cDNA clone S20T665307-4-F03
              5', mRNA sequence.
ACCESSION     BM818649
VERSION       BM818649.1  GI:19175062
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 396)
              Kim,M.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
              Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
              Oh,K.J.

TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags

JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics

Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: F column: 03
High quality sequence stop: 396.

FEATURES
Location/Qualifiers
    1..396
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone_lib="S20T665307-4-F03"
        /sex="M"
        /lab_host="Top10F"
        /clone_lib="S20T665307"
        /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
        Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
        bacterial alkaline phosphatase (BAP) and then dephapped
        with tabacco acid pyrophosphatase (TAP). The deapped
        intact mRNA was ligated with DNA-RNA linker including EcoR
        I site by treatment of T4 RNA ligase and the first strand
        cDNA was synthesized from oligo dt-selected mRNA by
        priming with dt-tailed vector. The dt-tailed vector was
        adjusted to have about 60nt. The cDNA vector was
        circularized with E. coli DNA ligase after digestion of
        EcoRI which site is also included in vector. An RNA strand
        converted to a DNA strand by Okayama-Berg method. The
        obtained cDNA vectors were used for transformation of
        competent cells E. coli Top10F, by electroporation method.
        The cDNA libraries constructed by this method are
        full-length enriched cDNA library."

ORIGIN
Query Match      100.0%; Score 18; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGGTTGAAGCGT 18
    |||||
Db 275 AACACGCGGTTGAAGCGT 258

RESULT 13
BI051278
LOCUS          BI051278          418 bp      mRNA      linear      EST 15-JUN-2001
DEFINITION    CM3-GN0297-110101-607-f03 GN0297 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BI051278
VERSION       BI051278.1  GI:14458808
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 418)
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.

TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags

JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics

```

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-
 110101-607-f03&t3=2001-01-11&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 418.
 Location/Qualifiers

FEATURES

1. .418
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="GN0297"

/note="Organ: placenta normal; Vector: puc18; Site 1:
 SmaI; Site 2: SmaI; A Mini-library was made by cloning
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the pUC 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 418;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AACGAGCGTTGAAGCGT 18
 |||||
 Db 84 AACGAGCGTTGAAGCGT 101

RESULT 14
 BM741875/c
 LOCUS
 DEFINITION K-EST0014589 S6SNU620 Homo sapiens cDNA clone S6SNU620-4-C01 5',
 mRNA sequence.

ACCESSION BM741875
 VERSION BM741875.1 GI:19063204
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 418)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS

Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 4 row: C column: 01

High quality sequence stop: 418.

Location/Qualifiers

1. .418

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S6SNU620-4-C01"

/sex="F"

/tissue_type="Ascites"

FEATURES

source

/cell_type="Scattering floating"
 /cell_line="SNU-620"
 /lab_host="Top10F"
 /clone_lib="S6SNU620"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 418;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AACGAGCGTTGAAGCGT 18
 |||||
 Db 147 AACGAGCGTTGAAGCGT 130

RESULT 15
 W01420/c

LOCUS

DEFINITION

z473d06.r1 Soares fetal_lung NbHL19W Homo sapiens cDNA clone

IMAGE:298187 5' similar to SW:BCIX_HUMAN Q07817 APOPTOSIS REGULATOR

BCL-X.; mRNA sequence.

ACCESSION W01420

VERSION W01420.1 GI:1273428

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 437)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.REGA+ET

High quality sequence stop: 383.

Location/Qualifiers

1. .437

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:1243109"

/db_xref="taxon:9606"

/clone="IMAGE:298187"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal_lung NbHL19W"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAGTGGAGCGCCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."

ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 437;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGAGCGTTGAAGCGT 18
 ||||||||||||||||
 Db 403 AACGAGCGTTGAAGCGT 386

Search completed: February 5, 2005, 08:11:53
 Job time : 2146.2 secs